

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

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From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Reed, Steven G.  
Krasny, Yacir A.W.  
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Campos-Melo, Antonio  
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(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
AND DIAGNOSIS OF TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 214

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: SEED and BERRY LLP  
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(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104-7092

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE: 01-OCT-1997  
(C) CLASSIFICATION:

## (vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 218121.411C7

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (206) 622-6958  
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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGACACG	GTACTTTGAA	CCAAACGCAC	AATCGACGGG	CAAAAGAAAG	GAAGACAGCA	60
ACCATGAAGA	TGTTGAATC	GATCGCGGCA	GCTCTGACGG	CGCGGGCTGC	AATCGGCGCC	120
GCTCGCGCCG	GTGTGACTTC	GATCATGGGT	CGCGGGGCGG	TGGTATAACA	GATCGAGGCC	180
TTGTTCTTGG	GCGCGGCACT	GCGTTTGGAC	CGCGCATCCG	CCCTTGAGGT	CGCGAGCGCC	240
GCCACTTTGA	CCAGCGCTGT	CAACAGCGTC	GCGGATCCCA	ACGTGTCCTT	TGCGAACBAG	300
GCGAGTGTGG	TGAGAGCGCG	CATCGGGGGC	ACCGAGGGGC	GCCTCGCGGA	CGACAGAGTG	360
AAGAAGCGCG	CGAGAGCGCG	GGATCTGCGG	CTCTGCTTCA	GCTTAAAGAA	CATCCAGCGG	420
GCGCGCGCGG	GTTCGGGACG	CGCGGAGGTT	TGCTCTCGG	GTTCGAGAGT	CTCGTCGCGG	480
CTCAGCGAGA	ACCTCAGGTT	GCTGAATCAA	CGCGGCTGGA	TGCTGTACCG	CGCTTCGCGG	540
ATGAGATTGC	TGAGAGCGCG	AGGCGAAGCT	ATTGCGGGGC	CGAGTTTACG	CGCGCTTCTA	600
GCTACGCGCG	CGCGCTGCTG	ACGCTGCGAT	GTTCAGAGCT	CGCGCTGCTA	GCACGATGCG	660
GTTCGCGGAG	GCGCGGCGCG	ACGCGCGGCT	GCGAGCGCTC	CTCGAGATAG	GTGCTGCTTC	720
CGCAGCGAGG	ACACCGCGCG	CGTGGCGGCT	TGCTGCTGCT	CGATCA		766

(2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGATGACCG	ATGATGACCG	CGATGACCG	CGATGACCG	CGATGACCG	CGATGACCG	86
GACTTCTGCA	CGATGACCG	CGATGACCG	CGATGACCG	CGATGACCG	CGATGACCG	120
GCGAGAGGCG	TGCGCGCGCG	CTCGCGCTTC	CTCGAGTCTA	AAGGAGGCGG	CGATGACCG	180
TGCGCGCTTC	TACTGACCG	ACCGATGACG	TGCGCGCTTC	GCGATGACCG	CGATGACCG	240
TTTCTGACCG	ACCGATGACG	GCGATGACCG	CGATGACCG	TGCGCGCTTC	CGATGACCG	300
TTTCTGACCG	TGATGACCG	GCGATGACCG	CGATGACCG	TGAGAGGCG	GCGATGACCG	360
TGCGCGCTTC	TGCGAGCGCG	CGATGACCG	CGATGACCG	AGCTGCGCTT	GCTGCTTTC	420
ACCGAGCGCG	AGAGAGCGCG	GATGACCGCG	ACGATGACCG	GCGATGACCG	CGATGACCG	480
GCGCGCGCTT	GCGCGCGCTT	TGATGACCG	GCGCGCTTC	ACGATGACCG	ACGATGACCG	540
CGCTGATGTC	CACGATGTC	AAGATGAT	TGCTGAGCG	CTGAGGCTC	CGCTGACCG	600
CGCGCGCGCG	CTGATGCGCG	GCTTACCG	CGATGACCG	CGATGACCG	CGATGACCG	660

TTGCNPAATC NTCTTCTCT GTGDNNAAG GGAACNTTAN CTTCGCGCTN GAAANGGTNA 720  
 TOUNGGGGCC NTCTTCTCT GGCCTTCTCT CT 750

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGATC ACCATACCA TCACACTTCT AACGGGCGAG CGCTCGGAG GCTCTGAGCA 60  
 CCACGGGAGA CCGGGGCGCA TCATCTCTCT AGCTTGAATC TGCTCAGGCA TGCTCTGAG 120  
 CAGCGGAGAG CCTATGTTT GTCTCTGACT CAGATATGCG GGAATTCGA TTCTCTGCT 180  
 GCGGCGGCGG GTCTCTGAA CTACTGCGAG AGGAATTTC AGCTGCGAT CAGATCTTC 240  
 ATCTGTCTCA GGTCTCTCT TTTCTCTGT TGTCTGCTG TGCTCAGGC CGGCTCAAG 300  
 ACCTACTCG AGGATTTGA AGGACCGAT AGCGGCGAG CTGCTGCTT TCAATCTTC 360  
 GACCGGCTT ACATATCA CATCTGCTG CCACTTACT ACCCGGCA GAGTCTGCT 420  
 GAATTTCA TCAGGAGAG GCGGAGAG TTCTCTGAG GCGGCTCT GTCTCTGCA 480  
 CGGAGGCGG CTCTGATTT GATATCAG TGCTCTGAG AGGATCTCG GATCTCTG 540  
 CTCTGATCG AGGCTCTCT GCTCAGGTC TACTCAGAG CGGCGGCG GCGGCTGAG 600  
 ACCAGTACA AGGCTCTCA TTGAGGCGG GCTATCTCA AGGATCTCG GATCTCTG 660  
 CTCTGAGAG CTCTGAGCA TCTCTGCGA GTCTCTCT CTCTCTCTG AGGATCTCT 720  
 GAGCTCTG GAGGAGCA AGGATCTG ATCTCTCTG AGGCTCTG TGGAGGCG 780  
 TGAATTTAT CAGCTCTCG AGTCTCTCA NAA 813

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGATATGAG AGGCGGCTT CAGATAACTT CAGCTCTG CAGGCTGCG AGGATCTCG 90

CATTCCGATC GGGCAGGCGA TGGCLATUC GGGCAGATC CGATCGGGTG GGGGTCACC	120
CACCGTTTAT ATCGGGCTA CCGCTTCTT CCGCTTGGT GTTCGCGACA ACACGGGCA	180
CGGGGACGA GTCCAGGCG TGGTGGGAG CGTCGGGCG SCRAATCTCS GCATCTCCAC	240
CGCGAGGTG ATCACCGCG TCGACGGCG TCGATCAGC TCGGGACCG CGATCGGGA	300
CGCGCTTAC GGGCATCAT CCGTGGGCT CATCTCGGT AATGGCAGA CGAAGTCGG	360
CGGCGCGCT ACAGGGAGC TGAATTGCG CGAGGACCG CCGGCTGAT TTGCTCGCG	420
ATACCGCGC CGCGCGGCG AATTGGA	480

(2) INFORMATION FOR SEQ ID NO:5:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCGACTGC GTCGCGGAG TATCTGCGC AGCAATGTC TGGAGCGCG CCAAGGAAT	60
CGGTCATCC GAGCTCGAG GTTCTGAGC CGCGCGCGG GGAAGTATCG GTCCATGCT	120
AGCGCGGCGA CGGCGAGCG CGGAATGCG CGATGAGCA GCGCGCGAT TTGCGCGGCG	180
CGGCGAGCG NGAGCGCGCG AATGCGCGA GTAGGAGGT GAGCATCAT GCGAGGCTG	240
ATCCGATGCA CTTGATTCG GCTGCGGCG CATTTGACA ATCAGGTAG TGACCGGCA	300
TGAATGATG AAAAGCGGCG GAGAGTCCG GTGTTCTGT GGTGTAGCT GCTGCTGCG	360
GTGNGGCTG ATCAGGATG TCTTGGGCA AAGCTGATC CGAGGAGAG GTGTGCTCG	420
NNANCCGAG GGTGTGCGN CCNNHHTCG TCGGCGATC CANAGAGCG GTGTATGCG	480
NAAAGGCTG GAGCAGGNN HATNGGCGN CCAAGGAGC HHHHGGGCG HHHHGGGCT	540
NNHHTTTCG ANHNNHHTG NHHHGGGCG NNCAGGCGN HHHHGGGCG HHHHGGGCT	600
NAAT	604

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 533 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCAGTCTG AACACCTCA CTAAGGGAA CAAAGGCTG AGTTCAGCG CGGTGGCGGC	60
CGCTGTAGAA CTAGTGAATH YYYKGGCTG CAGGAATYCG GYACGAGCAT TAGGACAGTC	120
TAACGGTCTCT GTACGGTGA TCGAATGAGC GAGGACATCC TGGTGATGGA CACCGAGGAA	180
CGGTGCGGAA CGCTCAGCTT CAACCGGCG CAGTCCGGA ACGCCCTCTC GCGCGCGTA	240
CGGATCGGT TTTTCGGHY GTTGGYCGAC GCGGAGGYCG ACCACGACAT CGAGTCTCTC	300
ATCTCTACGG GYCGGATCC GGTCTTCGCG GCGGACTGG ACCTCAAGCT AGCTGGCGCG	360
GCAGACCGCG CTGGCGGACA TCTACCGCG GTGGGCGCC ATGACCAAGC CGGTGATCGG	420
CGGATCAAC GCGCGCGCG TCGCGCGCG GGTGAACTG GCGTGTACT GCGACATCTT	480
GATCGGCTCC GAGCAGCGCG GCTTCGCGA CACCGCGCG CGGTGGCG TGGTCTCCAC	540
CTGGGACTC AGTGTCTCT TCGCGGAAA GGTGCGCAT GCGTGGCG GGTGATGAG	600
CGTACCGCG GACTACTCT CGTGACCGA CGC	633

## (2) INFORMATION FOR SEQ ID NO:7:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAG GCGCCGGAAG AGCGCGCGCG AACGGCGATC GACCGGCGCC TGCGGAGAT	60
CGGACACCTC CAGCGGAGAG TCGAATCATG AATTTCTGTA ACCATATTGA GCGCTGCGCG	120
CTCGCGGAG GCGGGGCGCC GGTGCGCGAG GTCTATGCG AGCGCGGCGG CGAGTTGCGC	180
CGGTGCGGCG AGCGCTGCG CATCTCTCTC GCGGAGAGG GACTGTCTGC GCGCGGCTGG	240
GCGACGTTTC GCGGAGACT GCTGCTGCGC GAGTGAAGG GTGCGCGTAA GGAAGCGGTC	300
GCGCGCGCGG TGCGGCGAG CCGCGCTGCG CCGTGGTGGC TGAGCGGACA CAGTACGATG	360
CTGTACGCGG CAGGCGAAG CGACAGCGCG GCGCGGATCT TGCGCGGCG AGCACTCTCC	420
GCGCGTACCG CGAAGCGCG GTATGTGCGG TGCGGCGGAG GAACCGGAGC ACCGCGGCGA	480
CGGTGCGTAC GCTTGGCGCC GAGTGTCTCC GCGGAATACC TGCGGAGCG GGTGCAATTC	540
GACTGTATCG CAGCGCTGCT CTGTGCTG TGAGCGGAAA CTTTCTGCG GCGGCGCGCG	600
GCGCGCGGAG AGTGTATCG CGCGGCGGCT GAGTGTCTCT TGCGCGGAAA GGTGCGCGCG	660
GAGCATGCGC CGGCGCGCTC CAGCGCGCG GTGAGCGCG GAGGCTGCG CGAGGATCTC	720

GCATGGGCGAA GACGGTCGGA GCGATAGCA AGCGCTTGG GCGGCTCAG CCACACCTG	786
GACACCGCGC CGCACCTGCC GCGACGACT CAGCAGTGC TCAGCGGCT CCGGGGCTG	840
TGGACGCGG AGCAATGCG GATGAGGCT CCGTGCAGG AGGAGACAC GCGGAGCTG	900
CGCGCTGAC TCGACGCGC CACCGCTCT GCGCTGCTA CCGCGCTGG CCGGCTGAG	960
GTGACCGAG AGGACCTGC CGCGGCGGA TCGCTGCTG ACACCGATG GCGCTGCTT	1020
GGCGCGCTG CCGGGCGCG CTCACCGCG GCGCGCGCA TCGGACCTG GATCGGCGC	1080
GCGCGCGAG GCGAGCTGC GCGCGGAGC CCGCTGCTT GAGTGTGCG GCGCTGCTG	1140
TAGGCTGCA TCGCTGCGC GAGGATCTC GCGCGCGGA AGGAGCTGG CGACAGGCT	1200
GCAAGCTGC CGGCTGCTT TCGCGCGGA GCGCTGCTT GCGCTGCTT TCGCGGCTT	1260
GCGCGCTG CCGCGCGCG GCGCTGCGC GAGGCTGAG CTCAGCTGC GCTGCGGAA	1320
GCGCGCGAG GCGCGCGCG GCGCGCTG GCGCGGAG AA	1362

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGCGC GCGATGCGC GCGAGCTAG CGAGGCTGT CCGGACGCA CTCGGGCGC	60
GTATGCTGC GCTTGAGGC ATCAGGACT GCGTGAGGC CCGCTGCGC GAGGCGCTC	120
TGATGAGCT GCGCGCTGT TACATGCTT ACXGCGCGC GCGCGCGAG CTCGGGAGC	180
CTAGGCGCTT GCTGCGCTG CGGAGGACT TAAAGCTGAG CTGCGGCGC CTGAGGCTT	240
TGCGGAGGC CTATCTGCT CAGGAGGAG AGGCGCGCG GCGGAGTGC AGGCGGAGC	300
TGATGAGGC ATCGGCGCG TGTGCGCGC CGGCGGAGC CCGGATGAG CCGGCTGCT	360
CGAGGCGCT GCGGAGGCG TTGCGGAGC TATACGCGA CCGGAGTTC CTGCGGAGT	420
GCGCGGCTT GATGAGCTT GCGGAGGAG TCGGAGTGT CCGGCGCTT TTTGCTGCT	480
GATGAGGAG TTGCGGAGC TCGGCTTTC CCGGCTGCG ACAGGCGCG GAGCTGAGC	540
GCGGAGGAG CGGAGGAGC TATGCTTTC GCGGCTGCG AGGCGGCGG GATGAGGCT	600
GCTGCGCGC CGGAGGAGC AGGAGGAGC TCGGCTTTC AGGCTGCTT GAGGAGGCG	660
GCGGCTGCTT CTGCGGCGC GCGGCGCGC GCGGCTTTC TATGCTGCT GATGAGGCT	720
GCGGCGCGC TATGCTGCT TCGGAGGAG AGGAGGAGC ATCGGCGCG GAGCTGCGC	780

ATTTCACCT	ATCGGTGGT	GTGACTGAG	CGTTCTGCG	GGCGTCGAA	CGACACGCC	848
TACACCGGT	GCTCAATCG	CGAACCGGA	AGATCGTGG	CGGATGCCC	GGCGCGAGC	900
TGTCGAGCG	CATCTGAAA	GGCGCGCAG	CGGTTGGGA	TCCGCGGCG	GTGTTTCTG	960
ACACGATGA	TAGGCGAAG	CGGTCGCGG	GGAGGGGCG	CATCGAGCG	ACCAACCGT	1020
GGGGGAGGT	CCCACTGCT	CTTACGAGT	CACTGTATG	CGGTCGATG	AACCTCGCC	1080
GGATGCTCG	CGACGTTGG	CTCGACTGG	ACCGATCGA	GGAGGTCGC	GCTGTGGCG	1140
TGGGTCTCT	TGTTGAGTC	ATCGATCTA	GGCGTACCG	CTTCCCGAG	CTGGGTGAG	1200
CGCGCGCGG	CACCGCGAG	ATCGGCTGG	GATCATGGG	TTGGCGGAA	CTGCTTGGC	1260
CACGTGTAT	TCCGTACAG	AGTGAAGAA	CGGTGGGTT	AGCGACCGG	CTCATGCTC	1320
GCATACAGC	GGGCGCGAG	ACGGCATCG	GGGCTTGGC	CGAAGCGCG	GGCGATTCG	1380
CGGCTTCAG	CGATACCGG	TTCGCGGCT	CGGCGCGAG	CGGCAACGA	CGGTCGCTT	1440
CGTCTCTCC	GACCGGCA					1458

## (2) INFORMATION FOR SEQ 10 NO:9:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (3) SEQUENCE DESCRIPTION: SEQ 10 NO:9:

ACGCTGTAAT	CTGCTGGAT	CTGGAGCGG	GTGGCGCGT	AGCTACGAG	ATCTACTGG	60
GGCGCGGGG	GGTGGCGCT	GGCATCGCG	TGCTGTAAT	CGGATGCTG	GTGGCGATG	120
TCTTCGCTT	CTTGAGAGC	AGCGCGGTT	CGAAGCGGT	CAGCGCGAG	AAGCGCGCT	180
CGCGCGAGG	CGATCGCGG	TGCGCGCAC	CGCGAGCGC	CGACCGGCT	GGCGAAGCG	240
AAGGTAAAG	CGCGCGGCT	CGCGCGAGG	CGCAAGCGT	CGAGACGCG	ACGCGCGCG	300
CGCGGTTGA	GGCGCGAGG	GTGCTCAGG	AAGCGCGAG	TGCGCGGAT	TGAGCGGCG	360
CGCTCAAGG	TTTACCAAG	CGCGCGAGT	ACTAGCTCG	CGACCGCGG	AAGTTCAAG	420
TGCTGTCAG	CAACATCGG	CTGCTGCTT	GTAAACCGA	CTTGGCGCG	GGGCTTTGG	480
CGGCTACTG	TTACTGCTG	GACACAGAG	GCTTGTGCT	CAAGCTGAG	TGCGCGGCT	540
CGATGAGAG	GCTGTCAGG	ACGTTTCTC	CGGTCAGCA	CGTAAGCGC	GGGTCAGCT	600
GGACCGGGG	GGGATGCGG	CGCGGCTGC	CATTGCGCG	CGCGCGGCT	GGGCGCGCA	660
CGTACATCT	CTGCTACAA	CTGCGGATC	TGCGCTGCT	CGCGGTTGG	TTCACTGCT	720



ATCAGCCGCC	GCGGCCGCC	GGACCGGTAC	CGGTCAGG	TCGAGGACAG	GCGCCTCCGC	740
CGGATCTCC	GCGCAGGG	CGATAATTAT	TCATCCGTGA	TGTCGATTC	CGGATCTGT	840
GACACCCCT	CGCTCGTCC	CG				862

## (2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 622 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: Linear

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA	GCGCAGAGC	ATCAGATCC	TCCCTGGGTA	TCGAGGTAC	CAATACAAA	60
GACACCGGG	GCGCAGAT	CTCGAAGTA	GTGCGGCTT	GTGCTGCCC	GAACCTGGA	120
GTGCGAAGG	GCTCTGTTT	CGCAAGATC	GACGACCCC	CGTCAACAG	CGCGAGCGG	180
TTGCTTCCC	CGTTCGGTC	CAAGCGCGG	GGGCCACAG	TGCGCTAAC	CTTTCAGAT	240
CGTTGGGAG	GTAGCGCAC	ACTCGAATC	AACTCGACA	AGCGGACCA	GTGATAGAG	300
TGCGCGGCA	GTCTTCAAG	CTGGATATA	CGTGGCAC	CATGACAG	CGTTCAGCT	360
TGCTGTTAG	CGCGCACTT	GTCTGCTG	TTCAGGATC	CACGCGCAC	GGCGATGAG	420
ACGACAGCG	GCGCTTTTC	ACCGAGTCC	TCACCGAGC	CGGTTTCTT	CTCAGCGCG	480
TGCTGCGCT	GTGCGGAGC	GAGTTCGAG	TCGCAATTC	CTCAACACA	CGGCTGATC	540
GCGGCTGAG	CTGCTGGCG	TCGCTGAGG	GCACCGGCT	GAGGCTGCG	GATCTACCC	600
CGGAGGCCA	CGGAGCACT	CT				622

## (2) INFORMATION FOR SEQ ID NO:11:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: Linear

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGCGGCG	TGAGCTGTT	GCGGCGGCG	ACGCTGCTG	TCAGAGCAT	CGCGGTGCG	60
ACCAACAGT	CGCTGTCAG	CGAGCGGCA	ACCTCTGCT	CGTTCAGCT	CGCGGCGAG	120
AGGAGCTCC	ACTCGAGCG	CTGACCGCA	CAGAAATG	CGTTCGACA	CTTCTGCTAT	180

GGTACGTCG	GATCGTGGC	GGGCTACGCG	TTGGCTACG	ACGCCAAGCG	GTCCGGTACC	240
GGGGTGACCG	AGTTTCTCAA	CAACGAAGCG	GATTTCGCG	GCTCGGATGT	CCCGTTGAAT	300
GGGTGACCG	GTCAACCTGA	CGGTGCGCG	GAGCGGTGCG	GTTCGCGCG	ATCGGACCTG	360
CGACGGTGT	TGGGCGCAT	CGGATCAGC	TACATATCA	AGGCGGTGAG	CACCGTGAAT	420
CTTGACGGAG	CGACTACCTC	CAAGATTTC	AAGGACCCA	TCACCGTGTG	GAATGATCCA	480
CAGATCCAG	CGCTACCTC	CGGACCGAG	CTGCCGCCAA	CACGATTAG	CGTTATCTTC	540
CGCAGCGACA	AGTCCGTAC	GTGAGCAAC	TTCCAGAAAT	ACCTGAGCG	TGTATCCGAC	600
GGGGCTTGG	GCAAGGCGC	CAGCGAAGC	TTACGCGGG	CGTGGGGCT	CGCGCGCGG	660
GGGACACAG	GAAGTCCGC	CTTACTGCG	ACGACGAGC	GGTCGATCG	CTACACGAG	720
TGTCGTTTG	CGGTGGGTAA	GCAGTTGAAC	ATGCGCCAGA	TCATGAGTC	GGCGGCTCG	780
GATCCAGTG	CGATCAGCG	CGATCGGTC	GGTAGACAA	TGCGCGGGC	CAGATGCTG	840
GGACAGGCA	AGACCTGGT	ATTGACGCG	TGTCGTTCT	ACAGACCCAG	CGACCTGCG	900
TCCTACCGA	TGTCGCTGG	GACCTATGAG	ATCGTCTGT	CGAATATCC	GGATCGGAG	960
ACGGCTACTG	CGTTAAGCG	CTTTATGCA	GCGCGATTG	GTCCAGGCA	AGAGGCTCT	1020
GACCAATAG	GCTCCATTCC	GTTCGCCAA	TGTTCCAA	CAGAAATTC	GGCGCGGCT	1080
AATGCTATT	CTTGACCTAG	TGAGCGGAT	TGACGCTGA	CGATGCGCT	TCCGAGGTA	1140
GCTCCGAT	TTGGCGGTA	TGAGCTATT	CGGCTGCTG	GCGAGGCGG	GATGCGGAG	1200

## (12) INFORMATION FOR SEQ ID NO:12:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCACACAGCT	GCAGGCTGTC	CTGTTGAGCG	AGCTGGGCTAT	GCGAAGACG	AAAGCACCA	60
AGACCGGCTA	CAACAGGAT	GCGACGCGC	TGAGTGGTT	GTTCGACAG	ACCGGCATC	120
CGTTTCTGCA	ACATCTGCTG	GCGACGCGG	AGCTACCGG	GCTCAAGGTC	ACCGTCAGC	180
CGTTTCTGCA	AGCGGTGGCG	GCGACGCGC	CGATCCAGAC	CAGCTTCAGC	CAGACGATCG	240
CGCGACCGG	CGGCTGTCG	TGACCGGAC	CGAAGCTGCA	GACATCGCG	ATCGCGACCG	300
ACCGCGCGCG	GCGGATCGG	GACGCGTTG	TGTCGCGGA	CGTTTACGCG	GAGTTGATGA	360
CGCGCGACTA	CAGCCAGTTC	GAGATCGCG	TGATGGGCA	CGTGTCCGCG	CACGAGCGCG	420

TCATCGAGGC GTTCAACACC GGGGAGGACC TGTATTGGT CGTGKXNTCC GGGGTCTTCG	480
GTGTGCCCAT CGACGAGGTC ACCGCGGGGT TGGCGCGCCG GGTCAAGGCG ATGTCTTACG	540
GGTGGTCTTA CGGTTTGAGC GCGTACGGCC TGTCCAGCA GTTGAATTC TCACCGAGG	600
AGGCAACGCA CGAGATGGAC GCGTATTTC CCGGATTCCG CGGGTGGCG GNCIACCTGC	660
GCGCGCTAGT CGAGCGGGCC CGCAGGAGC GTTACACCTC GAGGCTGCTG GCGCGTCCGC	720
GCTACCTGGC CGAGCTGGAC AGGAGCAACC GTCAATTCGG GAGGCGCGCC GAGCGGGCCG	780
GCGTGAACGC GCGGATCCAG GCGAGCGCGG CGGATATCAT CAAGGTGGCC ATGATCCAGG	840
TGCACAAGGC GGTCAACGAG GCACAGCTGG GGTCCGATAT GGTCTCTGCG GTCCAGGAGC	900
AGCTGCTGTT GGAATTCGCC CCGGTTGAAC GCGAGCGGTT CGAGGCGCTG GTGCGGACAC	960
AGATGGGCGG CGCTTACGCG CTGCACTTCC CGCTGGAGGT GTGGGTGGCG TACGGGCGCA	1020
GCTGGGAGCG GCGGCGGCGC TGGTGGCGGA GCTGCACTCT GGGGCGGCGA TTGCGGATTT	1080
TTTGGGCTTT GAGTTGAGCG TGGGCGGAT CGGAGCGGAG TTTGTCCAGC GTGTACCGGT	1140
CGAGTAGCTT GTCA	1156

## (2) INFORMATION FOR SEQ ID NO:13:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (1) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCGCTC TCGTGTCTTA AGGCTTTTAC CGGTGCGCAT CGGCGCGCGC GTTGGGAGTT	30
TGGGCGCTCG GCTTGGCGAT GGTCAACAG GTGTGCTCA ACCACGGGCG ATTGTGCGC	120
ATCGAGAGCA CGGACCGGCG CGGCGAGGCC CCGGGAAGTT CGATTACCTT GCTGCTCCCT	180
GCGCGTCCGA TCGCGATTCC GCGAGTTTCC GGTGCGAGCG GTGCGCTGCG GAGACCGGAC	240
ATCGAGAGCT CTGCGGCTTC GCGGAAGCTT ATCTCACTGA AATCTCAGTC CAGCGCGGCA	300
ACCTAGTTST GCGCTTACTG TTGAAAGCCA CAGCCATGCC AGTCCAGGCA TGGCGAGTTT	360
GCGCGGAGTA GTGGGCTTAC TACAGGAGCA GCAACCTAGC GAGATGAGCA ATACCGCGCG	420
GTATTGCGCA CGGCGCGAGC AGCGGGAAC CCGAGTTAT GGTCAAGGCG AGCAGCAAGC	480
GTACAGGAGC CAGTTGAGTT GCGTTTACCG ACGGTCCCGG CCGCGCGGCG GAGCCGAGTA	540
CGGTCAACCC TACGAGGAGT TGGGTGGTAC CGGCGCGGCT CAGATACCTG GGTGATTTCC	600
GACCTGAGCG GCGCTCTCTG GATGCTTTGG GTAAACGCGT CGTCCGCGCA TGTGGGAGAT	660

CGCCGCGGTC	ACGATAGCBB	TGGTGTCCGC	GGGATCGGG	GGGCGGGCG	CATCGGTGGT	720
GGGCTTCAC	CGGCGACCG	CGGGCCCGAC	CGGCGGGCCA	GTGGCTGCCA	GGCGGGGGCC	780
AAGCATCCGC	GGAGCAACA	TGCGCCCGGG	GTGGGTGGAA	CAGGTGGCG	CGAAGGTGGT	840
GGCGAGTGC	GTGATGTGG	AAACCGATCT	GGCGCGCCGC	TGGAGGAGGG	CGCTCGGGAT	900
CATTCTGTCT	CGCGAGGGCG	TGATTTGAC	CACCAACGAC	GTGATCGGG	CGCGCGCCAA	960
GGCTCCCTG	GGCAGTCCGC	CGCGAAAC	GACGTAACC	TCTCTGACG	GGCGACCGCG	1020
ACCGTTGAG	GTGTTGGGG	CTGACCGGAC	CAGTGTATG	GGCTCGTGC	GTGTTGACGG	1080
CGTCTCGGG	CTGACCGGCA	TCTCGGGG	TTCTCTCTCG	GGCTCGAGG	TGCTCTGCGC	1140
GGTCTGGCG	ATCGGCTCG	CGTCTGGTT	GGAGGGCACC	GTGACCGCG	GGATCTCTAG	1200
CGCTCTGAC	CGTCTGTTCT	CGCGACCGG	CGAGCGCGGC	AACGACAACT	CGTCTCTGGA	1260
CGCCATTGG	ACCGACCGCG	CGTCAACCG	CGTCACTCG	GGGGCGCGCG	TGCTGAACAT	1320
GAAGCTGCA	CTGCTCGGG	TGCACTCGCG	CATTGCCAGG	CTGGGGCGCG	ACTGAGCGGA	1380
TGCGCAGAG	GGCTCGATGG	GTCTGGGTT	TGCGATTGCA	GTGACCGAG	CGAGCGCAT	1440
CGCGCAGAG	TGATGACCA	CGGCAAGCG	GTGATGCG	TGCTGGGTG	TGAGGTGAG	1500
CATGACAAA	GACACCGCG	GGCGCAAGT	GTGCAAGTA	GTGGCTGGTG	GTGCTGGCGC	1560
GAAGCTGGA	GTGCGAAGG	GGCTCGTTCT	CGCAAGGTC	GACGACCGCG	CGATCAACAG	1620
CGCGACCGG	TGGTGTCCG	CGTGGCGTG	CAAGGCGCG	GGCGCGCGCG	TGCGGCTAAC	1680
CTTCAAGAT	CGCTGGGGCG	GTAGCGCGAC	AGTCAAGTC	ACCTCGGCGA	AGCGGAGGCA	1740
GTGATGAAG	TGGCGCGCA	GTGTTCAAG	C			1773

## (2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1958 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (4) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG	GTGGGGGGCG	GTCTAGAACT	AGTGGATGCC	CGGGGCTGCA	GGATTGGG	60
ACGAGGATCC	GAGTGGCGAG	GTCTGTAAC	CGGCGCGCG	GGAAGTATCG	GTCCATGCTT	120
AGCCCGGCGA	CGCGGAGCGC	CGGAATCGCG	CGAGTGAGGA	GGCGGGCAAT	TGGCGGGGGC	180
CGGCGAGCG	CGGCGCGCG	AGTGGCGCGA	GTGAGGAGCG	GGGAGTTCAT	GGCCAGCGTG	240
ATCCATGCA	CGTGCATTCC	CGCTCGGGCG	CGATTGACA	ATCGAGCTAG	TGAGCGCAAA	300

TGAATGATGG AAAAGGGGGG GTGAGGTGAG CTTTCTGGH GGTCGTAGGT GCTTGGCTGG	360
CGTTTGAGGT ATCAGGATGT TCTTGGGCGA AACCTGATGC CGAGGACAGG GGTTTCCCGG	420
TTAGCCCGAC GGGTTCGAGC CCGGGGTGCG TCGCGAGAT GAGGCGGTGG CTTGATGCCA	480
CRAAGGGGTT GAGCGAGGTC CAGCTAGCGG TCGGAACAC GCGGAAGTTC GAGAGGTTTC	540
TGGGTATTAC CAGTGGGAT GTGAGCGTCC GGGTGAATCG CCGCGGCGCA AAGGCGGTAT	600
GCACCTACAG CGACGAGCAG GGTGTCCGCT TTGCGGTACA AGGCTACAC ATCTGGGTGA	660
AACCTGTCGA CGACTGGAGC AATCTCGGCT CAGTTTCTGA ACTGTCACT TACGCGGTGC	720
TCGATCGTGC CGGTGGGTCG AGGAGCTGC TGTGGGTGT CAGGAACCTC CAAGCGGAAG	780
GTACCGAAGT GATGAGCGGA ATTTCGACCA CCAAGTCAAG GGGGACCATC CCGCGAGGCT	840
CTGTCAAGAT GCTTGAAGCT GGGGCTGAGA GTGGAAGGCC GCGGACCGTC TGGATGCCCC	900
AGGACGGTTC GCACCAAGCT GTGCGAGCGA GCATCGAGCT CGGATCCGAG TCGATTCCGC	960
TCACCGAGTC GAATCGGAGC GAGCGCGTCA AGGTGAGCTA GCGTGAAGTT CGGTGAGGCG	1020
GTTGTCGAA AGCGCGCTGT GAGCGGTGTC AAGGAGAC	1058

(2) INFORMATION FOR SEQ ID NO:15:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 542 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATTTCGCGA CGACAGCTGA TCGACATCAT GGGGACGAGC CCACATCCCT GCGACAGGCG	60
GGCGGCGGAG CGGCTCCGAG GCGCGCGCGA TAGGTCGAT GACATCCGCG TGCTTCGGGT	120
CATTGAGCAG GCGCTGCGCG TCGACAGTGC CGGCGAGATC ACCTACGCGA TCAAGCTCGA	180
AGTGTGCTTC AAGATGAGGC CGGCGCAGCC GCGTAGGCAC GCGCGCGCGA GCAAGACGCA	240
AATTCGCGAG GTTTCGGGTT GATTCTGTGG ATTTCGTGTC TGCTTCGCGA GCGCTACGAG	300
GCGCGCGCGA GATCCGCGTC CTGCGGTATC CAGGCGTCCA TCGCGATTTC GCGCGCGCGG	360
CGGCGGTATC TGCTTCGGGT CGACCGGAGC TGGCGGATTC GCGCGGAGCG TGATTCGATC	420
CGTGGCGGAG CCGCTCGATG CGCGAGTTTC CGGAGGAGAC GTCTTCGCGG CGGCTAGGGA	480
AGGCTTCGTA GCGCGCGGTC CTGACCGGCT GTGCTTCGCG GCTCGGTCGG GCGAGGAGGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 913 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGGCGGC CGCGCTTCCG TTGCCCCCAT TGGCCCGGTC GCGGATCAGC TGGCATATCG	60
CACCTTCAGC GCCTTTCGG CGGCGACGCG CGTGGGAGC GGGGCGCGCG ATGGCAGCGC	120
TTGACCTGG CGGCGGCGCG CGCATTTGCC ATACAGGAGC CGGCGGGGG CACCGTTACC	180
GGGTGCGCA CGGTGCGCG CGGTGCGGTT TGAGCGCGCG GAGCGCGAT GAACGCGCG	240
CAAGCGCGCG GCGGCGAGCG TTGGCGGTT TTGCGCGCG CGGCGCGCG CGGCGCATTC	300
CGGAACAGCC AGGCACTGTT GCGGCGAGCG CGGCGCGGAT TACCGCGCT GCGGCGCGCG	360
GCGCGCGGAC CGGCGATTAC CGCGGTTGCC GTTGGGTGCC CCGCGGTTAC GCGGCGCGCG	420
GTTCGCGCG AATATTTCGC GCGGCGCGCG AGACCGCGCG GCGGCGCGAT TCGCGCGCG	480
CACCGAACA ACAGCGCAAC GTTGGCGCG GCGCGCGCG TTGGCGCGAT CACCGCGAT	540
TGCGCGCGAG CAGCGGCTTT AATGTTTATG AAGCGCGTAC GCGGCGCGCG GCGCGATTG	600
CGGCGCGCG GAGCGGCTGC GCGCGCGCG CGGCAAGCG CAAAGCGCG CGGTTGCGAC	660
CGGCGCGCG GAGCGCGCG GTGCGCGCG TCGCGCGCT GCGCGCGCG GCGCGCGCG	720
TGCGGTGCT CAGCGCGTTA GCGCGCGTT GCGCGGTTG GCGCGGCGCG GCGCGCGCG	780
CGGCGCGCG GTTGGCGTAC AGGCGCGCG CCGCGCGCT GTTGGCGCG TTGCGCGCAT	840
TGCGCGCTT GCGCGCATTC GCGCGGTTCC GCGCGCGCG GCGCGGTTG GCGCGCGCG	900
GCGCGCGCG CGC	913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1812 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACCTTG GTGAGAAAA ATGCTGGCGC CGGAGCGCT AAGGCTGGGA CAATTCTGA	60
TAGCTACGCG GACACAGGGG GTTACGGGAT GAGGATTCG GCGCGCGCT CACTGAGGTG	120

GTGATGGTTC	CTGAGCGTGC	TGGCTGCCGT	CGGGCTGGGC	GTGGCTAGGG	CGGCGGCCCA	185
GGCGGCCCGG	CGGGCTTGTG	CGCAGGAGCG	GTTCGGCGAG	TTCGCGCGCC	TGCGGCTTGA	240
CGCTGCGCG	ATGCTGCGCC	AAGTGGGCTC	ACAGGTGGTC	AACATGAGCG	CGGAACTGGG	300
GTACACAAAC	CGCGTGGCGG	CGGGAGCGGG	CATCGTCATC	GATCGCAAGG	GTGCTGTGCT	360
GACCAATCAC	CAGCTGATCC	CGGGCGCCAC	CGACATCAAT	CGCTTCAGCG	TGCGCTCGGG	420
CGAAAGCTAC	CGGCTGATGC	TGGTGGCGTA	TGACCGGAGC	CAGGATGTCC	CGGTGCTGCA	480
GGTGGCGGCT	CGCGGTGGCC	TGCGGTGGCG	GGCGATGGGT	CGCGGCGTCC	CGGTGTGTTG	540
CGCGGTGCTC	CGGATGGCCA	ACAGGGGTGG	CGAGGGCGGA	ACGCGCGCTG	CGGTGCTTGG	600
CGGGGTGCTC	CGGCTGGGCG	AAAGCTGACA	GGGCTGGGAT	TGCTGAGCG	GTGCGGAGCA	660
GACATTTGAC	GGTGTGATCC	AGTTCGATGC	CGCAATGACG	CGCGGTGATT	CGGGCGGGCG	720
CGTGTGCAAC	GGCTAGGAGC	AGGTTGTTGG	TATGAGACCG	GGGGGTGGCG	ATAACTTCCA	780
GGTGTGCGAG	GGTGGCGAGG	GATTCGGGAT	TGCGATCGGG	CAGGGGATGG	GGATTCGGGG	840
CGAAATCGCA	TGGGTGGCGG	GGTCAAGCGC	CGTTGATATC	GGGGTACGG	CTTCTCTCGG	900
CTTGGGTGTT	GTGACACACA	ACGGCAACGG	CGCAGGATGC	GAAAGCGTGG	TGGGAAGCGG	960
TGCGGCGGCA	AGTCTCGGCA	TCTCCACCGG	CGAGGTGATC	ACCGCGGTGG	ACGGGCTTCC	1020
GATCAAGCTC	CGCAGCGCGA	TGAGGAGAGC	GTTAAGCGGG	CATGATCGCG	GTGAGGTGAT	1080
CTCGGTAAC	TGCGAAACCA	AGTGGGGCGG	CAAGCGTACA	GGGAACGTGA	GATTCGCGGA	1140
GGGAGCGCGG	GGCTGATTTC	TGCGGATAG	CAAGCGCGGG	CGGGCGAATT	GGATTGGGCG	1200
CAGCGGTGAT	TGCGGCTTGA	GGGCGCGAGT	TGCGTCTGCC	GTGCGGCTGG	CATTCTGAAA	1260
GCAATGAAAC	AGGCTGAGCA	CAGCTTTGAG	CAGCTTCCCG	TGAGGCGCAG	TTAGCTGAAA	1320
GGCGGTGTGG	TGAGGATATC	GGATGCAAG	GACTTCGCGA	CGCGCGCGCG	CTGCTCTGCC	1380
GATCGGAGCT	GTTTAAAGCA	CGCGCTTTTC	TAGGAGGTTC	TGGTGGCGCG	GTCTCTGAGC	1440
CGCAGCGCGG	ACGCTTCTGG	CGATCTGCGT	GGAGCTATGG	ATGCTCTGCA	GTACTTGCAG	1500
TGGTGTGGCA	TGAGTATGAT	CTCTTCCCGC	CGTCTCTAGC	ACTGAGCGGT	CGCGGAGGCG	1560
GCTTACGACA	TTGCGGACTT	GTACAAGGTC	CTGCGGCAAT	TGAGGAGCGT	CGAGGATTTC	1620
GTGCGCTTGG	TGAGGAGCGC	TGAGGAGCGA	GATATCGGCA	TGATGAGCGA	CGTCTGTGAT	1680
ATTCAGAGCT	CGAGGATGCA	CGCTTGGTTT	CGAGGATGCC	CGCGGAGCGC	AGAGGAGCGG	1740
TAGGCTGACT	ATTACGCTGG	GAGGAGGCTC	AGCGAGCGCT	ACAGGAGCGC	CGGATGATTC	1800
TTCTGTGACA	CGAGGAGGTC	GAGCTGCTCA	TTGATGCTGG	TGCGGAGGCA	GTGCTGATCG	1860
GGCTGATTC	TT					1872

(2) INFORMATION FOR SEQ ID NO:18:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1482 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTTCGCGGAA	ACCTGATGCG	GAGGAACAGG	GTGTTCCXCT	GGCGGCGACG	GCTCCGACCC	60
CCCGGTTTCT	CCCGCGATC	AGGCAATCGG	TGATGCGAC	AAAGGGGTTG	ACCACCGTGC	120
ACGTAGCGGT	CGGAACGACC	GGGAAGTGG	ACAGCTTGGT	GGGTATTACC	AGTCCCGATG	180
TGGAGCTCGG	GGCAATCCG	CTCGGGGCAA	AGGGCGTATG	CAGCTACAA	GGCGAGGAGG	240
GTGTCGCGTT	TGGGTACAA	GGCGACAA	TGTGGTGA	ACTGTTGAC	GACTGGAGCA	300
ATCTCGGCTC	GATTTCGAA	TTGTCAAGTT	CAGCGTGGT	CGATCCTGCC	GCTGGGGTGA	360
CGCAGCTGCT	GTGCGTGC	ACGAACCTCG	AGGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCA	CAAACTCAG	GGGACCATCG	CGCGAGCTC	TGTCAAGTGG	CTTGATCCCTG	480
GGCGCAAGAG	TGCAAGCGCG	GGCAAGCTGT	GGATTGCCA	GGCGGGCTCG	CACCACTGCG	540
TGGAGCGGAG	CATCGACCTC	GGATCCCGGT	CGATTGAGCT	CAGCGAGTGG	AAATGGAAAG	600
AACTCCCTCA	CGTGCATGAG	CGCGAAGTTG	CTTCGACGCG	TTGCTCCANA	CGGCTTTTGG	660
AAAGGTGTCA	ACCGGACCGG	AAAGCTGAGC	CGCTGACGCG	ATCTGMAAAT	TGACCGCCCTA	720
GGCGGGGCGG	TTGCTGGGTA	TTCTTCGGTG	GTTCGGGCTG	GTGGGAGCGG	CGCGAGCTCG	780
CGTCTTTTGA	CGCGGTAGCT	GTGCGCTCTG	ACGAGCGAGA	CTTCAGGCTG	GTGGACGAGA	840
CGGTGATCTA	TGGCGCGACG	AAGGAGCTCG	TGGCGCGCGA	AAAGTTTGGT	CGACCGGCGG	900
AAGGCTTAT	TGGAGCTGAG	GATCAAGCTG	CGCGGCTGCT	ACCGGGAGGA	CACCACTTGG	960
AAGAGAGGGT	TGGCGGCTTC	GGGCTCAAGC	GGATGTAGC	CGACTTCTTG	AATCAACAGG	1020
AGCGGATAGC	GGCGAAACCG	GGTGAATTCG	GGTAGATGCG	GGCGGGGCTG	GTCGAGCTCG	1080
GGGAACCGTG	CTACCAATTC	GGCGGCGGCTG	GGGAACGAGA	CGGATGCGCG	GGGCTGACAC	1140
GGGCTATGCG	CGAGGCGGAC	CGCAAGATGA	GTCTTCGCGG	TGCTAGGGCGG	GGCCCAAAA	1200
CAGGAGGTTA	TGGCGGCGCG	TTATGAAATC	CAGGCTGCGCG	AGATGTGCGG	TGCTGTGCGG	1260
TTTGAGGCGCA	CGAGCATGCT	CAAGTGGAA	CTCTTCGAGC	GACTTCGAGG	CGGGGAAGCG	1320
GGCGGCGCGG	ATCGGCGGCT	CGCGGCGGCTG	GGCTGCGCGG	GTGGAGGCTT	CGGCTGCGAG	1380
GGAGGCGGCG	AGGATATTCT	GGTGGCTGCA	GTCTGCGGCG	CGGCGCGGAT	CGGCGAGCGG	1440
GGACACTGAC	TGACCGGAGG	TGGGAGCTTT	CATTGCTTTT	GT		1482



## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA CGAGCCGGCC ATAGCTTCTG GCCCGCGGCC GACGAGATGG CTCGAGGGTT	60
CGTGTCTGGG GGCACGCGCG GGGGCACCAAC CTTGACGGGT GAGGGGCTTC AACAGCGCGA	120
CGTGCATCTG TTGCTGCTGG ACCGTACCAA CCGGGCGGTC GTTGCTTACG ACGCGGCTTT	180
CGCTACGAA ATCGCTTACA TGGGGAAGAC CGGACTGGCC AGGATGTGGC GGGAGAACCC	240
GGAGAACTTC TTCTTCTACA TCACCTTCTA CAACAGCCCG TACGTGCAGC GCGCGAGGCC	300
GGAGAACTTC GATCCGCGAG GCTGTCTGGG GGGTATCTAC CCGATTCAGC CCGCCACCGA	360
GCACGCGACC AACAGGNGC AGATCCTGGC CTCGCGGTA CGATCGCCCG CGCGCTTCCG	420
GGCAGCACAG ATGCTTGGCG CGGACTGGGA TTCTGCGGCC GACGTGTGCT CGGTGACGAG	480
TTGGGGCGAC CTAAACCCCG ACCGGGTGGT GATCGAGGCC GAGAAGCTCC GGCACCGGGA	540
TGGCGCGCGG GGGTCTCCCT AATTGACGAG AGCGCTGGAG AATGCTTGGC GCGCGGTGAT	600
CGCGGTCTCG GACTGGATGC GGGCGGTCCC CGACGAGATC CGACCTGGC TCGCGGCGAC	660
ATACCTCAGC TTGGGAGCG ACCGGTTCCG TTTTTCGAGC ATCGCGCCCG CGCTGCTTCC	720
TTACTTCAAG ACGGAGCGCG AATCCAGGCT TGGTTCGCGT TTGGGAGGCG GTTGGCGCGC	780
TGGACGGGTG AATATCGACC CATTCGCTGC CGTCTGTGGC CCGCCCGCCC ATTACCGCG	840
ATTGCGGCAA CGTGGGGGGT TGGCGCGGAG TAGGTT	876

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGCCCCCGG GCTCGCGGAA TTGGGCACGA GAGACAAAT TCGACGCTT AATGCAGGAA	60
CAGATTCTAA AGAATTAC ACCTGCACAA CAATATCTCC CGATCGGGGT TTATTTCGAC	120

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AGCGAAGACG TCCCGCAATT GCGAAGCAT TTTACAGCC AAGCGCTCGA GGCACGAAAC      188
CATGCAATTA TCTCTGTGCA ACACCTGCTC GACCGCGACC TTCTGTGCGA AATTCCTCGC      240
GTAGACACCG TCGCAACCA GTTCGACAGA CCCCGCGAGG CACTGCGCGT GCGCGTCGAT      300
CAAGAACGCA CAGTACCGA CCAATTCGCT CGGTTCACAG CGTGGCGCCG CGACGAGGAC      360
GATTTCCTCG GCGACAGATT CATCTAGTGG TCTTGGGAG AAGAGATCGA AGAGGTGCGC      420
TTGATGGCAA CCTCTGTGCG GGTTCGCCAT CGGCGCGGAG CCAACTGTT CGACCTAGAG      480
AACTTCGTGG CAGCTGAAAT GGATGTGGCG CCGCGCGCAT CAGCGCGCCG GAGCGCTGCG      540
GGGGCGCCCG TCTAGATGCG TGGCGGGAAT CAGCGAGTGG TCCCTTTCG CCGCGCTGCT      600
TCCAGCGAGG CGTTCGTGCG CCGCGAGTGG TGAGTACCAA TCGAGGAGC CCGCGAGTGC      660
CGGAAAGAT CGATGCTCTC GTACTGCTCG AGCTTCGAGG AGTACACCG CCGCGCTGTA      720
GCTCGCGAGG GGTCAACGAG TTGCGGATAT TCTTTAAGG CAGCGAGTGA GGTCTCCAGC      780
CGGTTCGCGC CACCGCGCGT GCGCGCACTG CTGCTCAGGT ATCGGGGGGT CTTCGCGAGC      840
ACGACGCTCG GCGAGAGGAG TGGAGCGCGC CGGATCCGCA GACCGCGGAG CGGAAACGCA      900
CATCACACCG CGACGAGATC GATCTCGGGA GGGGGTGGG GGAATACCGA ACGGTGAGG      960
GAGCGCGAGG AGTGTGTTT CCACGAGCGA AGCTTTTCG GGTCACTGCG GCGNTTTAAG     1020
T                                                                                   1021

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(2) INFORMATION FOR SEQ ID NO:21:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[X1] SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

GCTCGCGAGG AACGGAAGAA CACAACCTGG AGATGCTGA ATGATGTCG CGTAGGCTTG      60
ACCGCCCGCG CTGCAATGCG CGCGGTTGGG GCGGCTGGA CTTCGATCAT GCGTGGCGCG      120
CGGTCGTAT AACAGATGCA GCGGTCTCTC TTGAGCGCGC CACTGCGCTT GCGCGCGGAA      180
TGGGAGGCTG AATGTCGAG CCGCGCGCGG TGGACCGAGC TGCTGAGAG GGTGCGCGCT      240
CGCAACGCTG CTATTGAGAA CAGCGGACT CTGCTGAGG GCGGATGCG NGGAGCGAG      300
GCGGAGATC GCGAGACAA A

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(2) INFORMATION FOR SEQ ID NO:22:

- (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (1) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCGGTTTSC GACGGTTTT GCGNCGGGT GGTATCCDS CTGGGCCAGC	60
CGATGACGG GCGGCGAAC GTGACTTCG ATACTCGGC GCGCTGGAG CTGAGGSC	120
CGTCGTCTT GACCGGCA GCGTGAAG AGCGTTGA GACCGGATC AGCGGATTC	180
AGCGATGAC CGGATCGGC GCGGCGAGC GCGACTGAT CATCGGGAG CGGAGAGCG	240
GCAAAACCG CGCTCTGT GCGACACAT CCGCAACTA GCGGAGAGA CTGAGACTCC	300
GGTGAGTCC AAGAGGAGS TCGCTTCTG TATAGTTTC CCATCGGCA AGAGGGGAA	360
CTTACCATCG CGC	373

## (2) INFORMATION FOR SEQ ID NO:23:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (1) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGACGCGGT GATGGGATTC CTGGGCGGGC CGGCTCGCT GCGGTTGTC GATCAGCAAC	60
TGGTATCCG GGTGCCCAA GCTGCTCTT TTGCTCAGC AGCGCTGTC CGCTGCTTT	120
TCITGACGC CTGGTACGG TTGCGGATT TACCCGAT CAAGCGGCG GAATCGGTC	180
TGATCGATC CGGTACGCG GGTGCGGA TGGGCTTCT GCGCTGCTT GCGGCTGCG	240
CGGTGAGCT TTTCGTCAC CCGAGCGTC GAACTGGA CAGCTGCTC GCGATGCTT	300
TTGAGACGA ACCATACCG NGATTCCCN ACATGCGAG TTGCGAGGA GA	352

## (2) INFORMATION FOR SEQ ID NO:24:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG	TTGATTCCTT	TGACACAGCG	GCTGCGGATG	ATGACGGAAG	TGATGAGGCT	60
GCGGTTCGCG	GGGTTCATGG	GTACACGCGA	GTAATCAGCA	AGTTCTCTGG	TATATGCCAG	120
CTAGCGTCCA	GTTCCTTGCC	AGATGCTTTT	CTGACGCTGA	TGGCATGTAC	CGGTTCGCTT	180
GCCTGAGCT	CATGCTGCG	GGTGCATCC	TGGGACGCG	TGTGGCGGCT	CTCGGGGTCG	240
GCCTGAGCT	CGCAGCGCA	ACCGCGCGG	TGCGCGCTA	CTACTGCTGC	CGCGGGCAGC	300
CTTTGACCC	CGGATGGGG	CGCACTTGG	ATGCTTACAC	CTGCGATGAC	GACTTCCACC	360
CGGATGCGA	CGCGCTGAC	CACAGCGCG	ACTAGCGCG	AGGATGCTC	GAAGGTCCCG	420
TGCTTGCGA	TGCGGTGCT	GCGCGCGCG	CGCGCGCTC	CGGTGGCGCG	GCATGCGCT	480
CGTTGAGCG	CGCGGATGG	CGAATAGCG	TATAAGCGG	GGCGTCCCG	CGGCAAGCTA	540
CGACGCGCG	CGCGGCGAT	TTAGCGTCT	GTGCGGATG	ATCGCGCGCT	CGGATGACG	600
AAATAGCGG	AGGCTTTGG	CAGCGCGCT	CAGGAGCGCT	GAAGGAGAC	TGCTATGAC	660
GGCGGCGCG	CGTGCACAT	CGGATGCGG	AGGCTGCTT	CGCGGAGAC	CTTTCGCGG	720
ATCGTG						726

## (2) INFORMATION FOR SEQ ID NO:25:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGGCGCG	AGGATGCTG	GGCGGCGCG	CGCGTATGCG	TTGATGAGG	CGCGGCGGAT	60
GCTGCGCGAG	CATATGAGG	CATGCTGCT	GCGGCTGAG	CGGCTTTTG	AGCGGCGCGG	120
CTGCGGATG	CGCGGCGCT	GAGTCTATT	CGCGGCGCT	TGTGCGGCT	ATGAGCGGGA	180
ATAGGAGCA	ATAGGAGGAT	GATTTGCGAG	TTCATGCTG	GATATGCTG	GAATGCAAT	240
GGCGGCGCG	CGCGGCGCG	GAGCGGCTG	CGCGGCGCG	CGCGGCGCG	ATGCGGAGG	300
AGGCTCAT	CGCGGCGCT	AGCGGCGCG	CGCGGCGCG	TGCTTTGAG	CGGATGAGG	360
AGGCGCGCG	CATGCTGCT	CGGATGCGG	TTGCGGCTG	CGGCGGCTG	GTGCGGAGG	420
TGCGGCGCG	CGGCGGCGG	GAGTCTGCT	AGGATGCGG	AGGCTTACT	AGCTGAGAGC	480
AGCGGCGCG	CGGATGCTG	GCTGCGCGG	CAGGCTTCT	GCTAGCTCT	CAGTCTCTG	540
TGCGGAGCT	ATGCGGAGG	GAGTCTGCT	ATGCGGCT			580

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCC CGCGGGTTT TGGCGGGGC GGGCGGTTC GGGGCAAGG GGGGCGGCC	60
GGTACCGGCC GTTTTTCGG TGTGGGGGG GCGGTGGG CGGAGGCA CGGATCGGC	120
GGTGTCAAG GTACGTGGG CAGCAGCCG GTGATCCG	160

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACGATA GATGTTGT GTACGGCAAC GTTGTGACA CGTCCAGGC GTTCAGATC	60
CAGCGGCAC CCGCGCGGT GAGCATGGT GATGGGCC GTTTCGGA GCGGGTGGC	120
AAGCGATGG GAATCGACA GTTGGGGTA ATTCATACG GAATGGACC GTTGTGCT	180
GACCGGAAAC AATGGAGCA CGCAACCAAC AGCTTGGGT TGGCGCGGG TGTGTTGTG	240
GGTACGAGC GAGCGTACA GAGCAACCC CG	272

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGGGGTT GTTTCGGAC TATGCGGCA CGGTGAGCA GCGGAGTTC CGCGAGTGA	60
AGCGATCGA CGACAGGAT CGGTGCGCG GTTCAATGC CTAGTGGG GATATACCG	120

CCGACGAGCT GAGCGTGGCC GAGCGGGGGG GGGTCATGGG GGTGGATGGG GGCACGRTCC	180
GTTCGGATCT GCGGTGGTTC GAGACCGCTC ATCTGCTACA TCGGCTGGCC GCGTGGTGGG	240
GGATCTGAC CGGAGAGATC AAGAGCGGCT CAAAGATCCA GCTGCTGGAG ACTGGGTTTG	300
CGGCTTGGTT GCGGGGG	317

## (2) INFORMATION FOR SEQ ID NO:29:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTGGAG CTGTGATGA ACAGCTTGC CGGACGGCG GCGGCCAGCA CGTGGTGTG	60
GCAGGTGGG ACCACTGCG CGGTGGGAG CATGGTATC ACCACGTGG CCGGGGCCAC	120
CGCTTGGCG GCGCTAGAA ACAGCGGAG AGGTGGCGG GCGGGGCGG AGCGCGGCT	180
GG	192

## (2) INFORMATION FOR SEQ ID NO:30:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATGCGAAG TTTGCTGAG AGGTGCTGA CGGAAAGTC TGGGGGCTG CGAGCGGGT	60
CGGCTTCAZ CAGGGAAGA CAGGCTGTC CAGCTGCTC CGGCTGCTT ACGCGGGCA	120
GAGGTTTGA TTGCGGCGG CGGCGAGCG GTAGCAAGC TTGGGCGCT GCTCTCTAT	180
GAGACTCGG GGTAGGCAAT TGACCATGG GTGTACCGG TCGCGAGCA TTGAGAGCT	240
CGGTGTGAG ACCAGCTTCT CGAGCGCTT CAGCGGTGA GCGGTACCT ATGAGACCC	300
ACGTTGG	308

## (2) INFORMATION FOR SEQ ID NO:31:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACGACGAG GCAACTCAGG TGGATGATGG TCGGACGGG CATTCAGGAC GGAGAGATTC	60
CGCCCGAAGC TCGCCGGGG CAAGTCTCTA TASTGACCGG CCGTAGAGGG CTCCCCCGAT	120
GGACCCGAC TATCTCTGGG TCGCGCTGGC CGGTAAAGAG GGTAAAGAGA ATGTGAGGGG	180
ACACGATGAG CAATCACGCC TACCGACTCA TGGAGATGGT CGGACCTCG CCCGACGGG	240
TCGACGGGG AATCCAGGG GGTCTGG	267

## (2) INFORMATION FOR SEQ ID NO:32:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (x2) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCTGCCGA AAGATGTGA CGGACAGCA TGACCATCA CAGTACCGA GTGATCGAG	60
TGCTGGGAC CTCGGCGAC GCGCTCGAG CGGCACTCA GCGGGTCTG GCCCGACTT	120
CGCGACCAT GCGCGCTCG GACTGGTTG AGTACAGTC AATTGAGGC CACCTGGTGG	180
ACGGAGCGGT CGGCACTTC GAGTGGACTA TGAAGTGG CTTCGGCTGG AGGATTCTGT	240
AACCTTCAG CGCGGCGAT AACTGAGGT CATCATTAAG CGACTTTTCC AGAGATCCT	300
GAGGGCTCG AAACCGGTT CAGCGAGCG TGGCTCGGC GAGGCTCTG CTCGAAATC	360
CTTCGGAGAA TTCTCGGGG GCGCTTACA GGAATGGGT GTTGAATTC TGGGTATCT	420
GCTGACCTG TGTGGCGTGG AGCGGAGCA AGCGTCTG GACCTCGCT GCGGCTCGG	480
GCGGATGGG TTGCGCTCA CCGCTATCT GAAACGGAG GAGACCTAG CGGCTCTGA	540
TATCTCGAG AAAGCGATCG CTGCTTCCA GAGGCATC ACCTCGGGG AGCGCACTT	600
CGAGTTCAG GTCTCGACA TGTACAATC GGTATACAG CGGAAAGGA AATACCGTC	660
ACTGACTTT CGCTTTCAT ATCGGATGC GTCTTTCAT GTGTTGTTT TACCTCGGT	720
CTTACCCAC ATGTTTCTG CGGAGTGGG GCATATCTG GACGATCTT CGCGCTCTT	780
GAGCGCGGC GAGGATGTC TGTGACATA TTCTCTGTC ATGACGAGT CATTAGCCA	840
CATTCGGAA GGAAGAGTGG GCAAGACTT CGAGATGAG GACCGGGTT ATCGGCAAT	900

CCACAGAGAG CAGCCGGAAG AGGCAATCGG CTTGCGGAG AGCTTCTCTA GGGATGTCTA	950
TGCAAGTTC GCGCTCGCGG TGCACGAGCC ATTGCCTAC GGTCTATGCA GTGCGCGGA	1020
ACCACGCTTA AGCTTCGAGG ACATGCTGAT CGGATCAAA AGCGGAGCT AGTTCGCTAT	1080
CGGGAGAGCA TCGGACATCC GTGGGCGGCA GGGCGCTGC CGGAGGCTG ATTAGCGGG	1140
CAGATTAGCC GCGCGCGCT CCGGCTCTCG AGTAGCGGCG CCGATTTGGG GTACCGCGCT	1200
GCTAACCGCG GTTGGGCGCG TGGGGGCGCG CTGCGCGAT CAGGTGGTAG ATCGCGGCA	1260
AGCGTTCGCT ATCGCTCAT ACCAGCGGCG AGAGCGGCG GTTGTGCGCC AGCGCGAGCG	1320
CGACCGCGGT CTCGCGCTCT GTGAGCGCA TCGAGCGCG CAAGCGGCA TGACGAGAG	1380
CGCGATCGG GTTGGGCGCG GCGATACGCT GATGCGGAG ATGAAATTT AAGGCGGCA	1440
ATAGATTTCG ATCGCGGCA GTTGTGCTG GGTGCGGCT CAGGCGGCG AGGAGCTCG	1500
CGGCGAGAG CGATGCGCG TCGATCTCG CTCGCGCG	1539

## (2) INFORMATION FOR SEQ ID NO:33:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (3a) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCGGCTG GGTGATGGA GCTTACCGG GGGCGAGCG GAGCTAGCG CGGCGAGCT	60
CGGGCTTCT CCGCGGCTT AGAGAGCGG GTATGCGCT AGGTGCGCG CGGCGGCTG	120
CGCGAGAGC CGTCTCGAG TGATGCTCT GATAGCGCG AACCTCTGG GCGAGAGAG	180
CGCGGCGAT CGGTTCAGG AGCGCGATA CGGCGAGAT TGGGCGGAG AGCGCGGCG	240
GATGTTTGG TACGCGCGG CGAGGCGAG GCGAGCGG AGTTCTCTG GTTTCAGGA	300
GGCGCGGAG ATGAGCGAG CGGTGCGCT CTTCGAGAG GCGCGCGCG TCGAGAGAG	360
CTCGAGAGC GGTGCGGCA AGGATGCTT GAGATGCTT CCGAGCGCG TCGAGAGAG	420
GGCGAGGCG AGCGAGGCA CGAGCGCTT TTGAGAGCG GGTGCGCTT GAGAGAGAG	480
CTCGCGGAT GGTGCGGCA TCGAGAGAT GGTGCGGAG GCGAGAGAG AGTGTGAGT	540
GAGAGAGAG GGTGCGGCA TCGAGAGAG CTGAGAGAG ATGTTGAGAG GTTGTGAGT	600
GGGCGGCGG CGCGAGGCG TCGAGAGAG GCGAGAGAG GGTGCGGAG GTTGTGAGT	660
GCTGCGGAG TCGTGGGCT CTGCGGCTT GCGCGGCGG GTGCGGCGG AGTGTGAGT	720
CGCGGCTGAT TCGCGGAGT TCGAGAGAG TCGAGAGAG TCGAGAGAG GTTGTGAGT	780



GAACGGTGGT CCGGCGTAAG GTTACCCCC GTTTCGTGA TGGGTGAAC TTGTCGAAG	840
GAACAGTGA C	851

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTGTGTCGG GCGGAATTT GGACCGATT CCGCTCCGG GATAACCCA TCATCGAAC	60
CTAGATTAT TCGTCCAGG GCGCCGAGTA ATGCTCGCA GAGAGGAAC CTACTCTCG	120
GGGCACTGT TGTAGTTC TCGATAGGG GGAAGGCTC GACATTTTC ACAGACACC	180
CCATCAAA GTTCGAGGC CACTCAGCT TGTAGGAGG GCGACCGAT CGCAGGCTC	240
GCTTCGTCAA GATC	254

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1227 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATTCGTACC GAAGCGGCG CCGCGAGGC GAATCGTG TTGACCGAG AGGAGCGGA	60
CGATCTGGCG CTGCGATCG CGGTCAGGC GGGGGGGTGC GCTGATTGC GCTATAACT	120
TTCTTCGAC GACCGGAGCG TGAAGGTGA CCAAGCGCG GAGTCGGTG GTTTCAGTT	180
GATCGTGGC CGGATAGCG GCGGCTATGT GGAAGCGCG TCGATGATT TGTTCGACG	240
TATTGAGAG CAAGGTCAC CATCGCAAT CCAAGCGCG CGGCTCTG GCGTTCGGG	300
GATTCGTCG ACTGATAGA CGCTAGTAC ACCCGCGGT GCGCAGACG TACGAGACA	360
CCAGAGCTG ACCCGCTGG AAAAGCACT GAGCGATGC TTGACCTGA CCGGTTGGG	420
GCGCGCGCG GCGAGGTGC ACTGCATG TGAACAGCG CTGCGCTGA TATTGCGGC	480
ACTACAGAT TTTTCGATG GAGTCACTT CGGCTGGA GACTGCTTG CGAAGGCTT	540
CGCTGCTCG CTTCGCAAG GCTGATCGG AGGCTTGT GCGACGCG TGTGAGATC	600

CCGACAGCCG	ATTCGGAACG	ATGGTGTCCA	CATCTCGGTT	CTCCAGCCCG	TTGAGGTATC	660
CCTGAAATCG	GGTTTGGCCG	GGTGCTCTCG	AAATGTGCC	TGCGGTGTTC	GCTCCGTTGG	720
TGCGGACGCG	CTATATGATC	GCGGCGCTCA	TAGCGGACAC	CAGCGGAGCG	GCTACACAAA	780
TGCGGATCAG	CAGCGGCTTG	TGCGGTGCTT	TGCGGTAGGA	CAGCTGCGCG	GGGAGGCGCG	840
GATATCGCGG	GGCGGCGAGC	GCGGCTGTCT	CTGCGGTTCC	CGGCGGAGAG	GCGGTTTGGG	900
CGCGGCGGAG	GTCGTGGGGG	TAGTCCAGGG	CTTGGGGATC	GTGGGATGAC	GCTCGGGGTT	960
AGCGGCGCGG	TGCGTTGGTG	CGGACACCGG	GGTTGGGCGA	GTGGGAGCGG	GGGATTGTGG	1020
TTCTCTTAGG	GTCGTGGAGG	GGACAGCTG	CTAGGGGAGC	AACCGCGGCT	CGGCTCAGCC	1080
GGGAGCATGG	GCAATCAGGT	GAGTCTCTTA	GGGAGGCTAG	CGCAAGCTCT	GCGGTAGCTT	1140
CTCAAGCGCA	CGGCGCGGCG	CGCGGCGCGG	ATAATGTTCG	AAGACTAGGG	AACCTTAGGG	1200
ACGAGGAGCG	GAGATTITTT	GACGATC				1227

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGTTGTGCG	CGGATCGGCG	GGGTGGTTGA	ACGSCACGCG	CGGCGCGCGG	GGGCGCGCGG	60
GGACCGCGCT	TAGGCTGTGT	GCGGCGCGCA	AGGCTGTGTT	CTTGGGCGCG	GGGCGGTACG	120
GGGCGCGCGG	CAGCATGTGT	GGGTTGCGCG	GGTGGGCGCG	ATTGTCTTAC	GGCAACGCGG	180
G						181

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTTGTGCG	CGGATCGGCG	GGGTGGTTGA	ACGSCACGCG	CGGCGCGCGG	GGGCGCGCGG	60
GGGACCGCGT	CTTGGCTGTG	GCGGCGCGCG	AGGCGCGCGT	CTTGGGCGCG	GGGCGGAGATG	120

CGGACGGCTC CACCGGCGC AACGGCGTC TTGGGGCGT GGGGGGTGCG GGAGGCACG	180
CCCCGGGCGG CGGCTTGGGT GGCACGGCGG GTAGGGTGG CCGGCGCGG ATTGCGGGCG	240
GCCTCAGAG CGGACGGCGG CTGGGGGTG AGCGCGGTGA CGGGGTGAC	290

## (2) INFORMATION FOR SEQ ID NO:38:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCAGTGG CATGNGGGT GTGCTGGAA GCT	34
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## (2) INFORMATION FOR SEQ ID NO:39:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGTGCT GTGCCCCCGG TTGCGCGCGA GCGACCGGT CCGACGTTA CCGACAGG	60
TTGGGTGTC GCGAGTACC CCGGACCGG CGACCGCGA GTCAACAAAT GGCACGCTG	120
TATCCCCAG ATGCGCGCG GCGACCGG GACCG	155

## (2) INFORMATION FOR SEQ ID NO:40:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGACGTCA CGGCGCGCG GCGACCGCG AGCGCGGCG GCGCGCGCG TGG	53
---	----

## (2) INFORMATION FOR SEQ ID NO:41:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCGACCGG GAGTGACAGC GGTGCCCGTG GCGCCACCCC GACCAGCGGC GGCACGCGGC	60
GCACCGCGCG CAAAGCGCGC AACGCCACCG TCTCCGCGGC GCGCGCGCGG CCGCGCGCGC	120
AGGGCGCGCA CG	132

## (2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGCGCGC CGGACCGGNC GGGGACGGCG GTACGGCGCG NAAAGCGGCG GCGGACGCGC	60
CGGCGCAGCA ATCTCCGCGG TCNCGCATG GCGCGCATCG CGGACGCGCG GGCACGCGCG	120
GCNCGCGCGC CA	132

## (2) INFORMATION FOR SEQ ID NO:43:

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCGCGGAG ATCGGTACCG CCGCGCATCG GCGCGCGCGG ATTCGCGCGG TTTCGCGCGG	60
CGAGGAGAGG CGGTACCGCA TGGCGCTGCC GAAGTAGCGG GATCGGTTCC CGATGCGCGG	120
ATGACGCGCG GGCATCAAGT TATGCGAGGA ACCTTCAGT TTAGCGAGCA TAATGCGCTAT	180
AGCGCTAAGG AGATGATGCG GATATGACCG AGTCGCGAGC CGTGACGGTG GATCAGCGAG	240
AGATTTTGAA CAGCGCCACG GAGGTGGAGG CCGCGATGCG GGACCGCGCG ACTGATGCGG	300
CGATCACCGC GTGCGAATTC ACGCGGNTA AAACCGCGCG CGAAGCGTGG GTNTTGTGTCG	360

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CCGACACAT  CCGGGAATAC  CTGCGGGGCG  GTCCAAAGG  GCGCAGCGT  CTGCGGACCT  420
CGCTGCGCA  CGCTGGCGAG  GGGTATGCG  AGGTTGATG  GCGGCTCGG  ACCCGCTGG  480
ACACGACGG  CGAAGGACT  GTCCAGGCG  AATCGCCCG  GCGGCTCGG  GCGGACGTT  540
CGCCGGAAT  AACGATACG  CGAGGGGCG  CACGCGCGG  TGAACCTAC  TTCTGCGTC  600
TCAGACAGG  GCGAGGAG  CTCGAAAGG  GCGACCAAG  CGATCGCTC  GCGGCTCGG  660
GCGTGGGTC  GACGCTTC  ACCCTGAGC  TCGAGGCG  CG  702

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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

GAAGCGGAG  CGCTGCGCG  GACCTGGCG  GTCAAGCGG  CATCGCTCG  TGCGGTCGA  60
GCGGCGGGG  TGCGTGGCG  GCGGTTGGG  TGCGGATCG  GCGGTCGCG  ATCGCTGCG  120
CGCGTGGCG  CTGCTGACAT  TGCGGCTTA  GCGGCGGAA  GCGGCGCGG  CGCGCGCGG  180
CTGCGCGCG  GTGCGATGG  AATGCGGAT  GCGCGCGCG  ATCGGCGCA  AGCGGCGCG  240
AAGCGAAG  GTTCTGAG  GCGAGCGAG  GCGCTTACA  CGGAGGATC  TCGTGGCG  296

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CGGCGAGGG  ATCGAATCG  GTGCGCGGA  GCGACCGTC  GCGTCGACC  ACTGAGGAG  60
CGCGACCTA  CTGCGCGGT  AACCGCGAT  ACCCGGAGC  GCGCGCGCA  GCGTCTTAC  120
GAGCGTCAG  ACCCTGCTC  GCGCGCGCG  ATGAGCGTC  GCGGAGCTA  CGGATGAC  180
TGAGCTCGC  GGTGCGGTC  CTGCGCTCG  CTGCGTACT  GCGGCGTTC  GCGGAGTGT  240
TCGCGCTCG  TACCGAATC  GCGGCGGTC  ATGCGCGCT  GCGCGTAC  ACTGCGCTC  300
CGGCGCGGT  GCGTCTGTC  GCGCGCGTC  TTGCGCGGT  GGTCTGCTG  CGTAAAGCG  360

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AGAGGACATGT GACGGTACTTT GGGGTGGTCTG GGGTACTCGG CGTATTTCGT AIGGTCTCGG	420
GGAGCTTTAA CAAGCCCRGC GCGTATTGGA CCGGTTGGGC ATTGGGGTT GTTTTGAATT	450
TCATCGTGTT CCAGGGGGTT GGGGCAGTCC TGGGCTCTT GGTGAGAGCC GGGGCTATCA	540
CGGCGGAGC GGGGCGGGC AAGTTCGACC CATTATGACA GTACGGGGG TACGGGCAGT	600
AGGGGCACTA CCGGTCGAG CCGGCTGGT ACTATGTC CAAGGGTGT CAGCAGGCGC	660
CGGGACTGCA GTGGGGGGC CCGGCGCAGT CTCGCGAGCC TCGGGATAT GGGTGGCAGT	720
AGCGGGGCTA TTGCTCGAGT CCGAGCGAAT CCGGCGAGTC ATACACTGCT CAGCGCGCGG	780
CGGAGCGGCC CCGGCGAGTCC GGGTCGCAAC ATGCGAACCA GGGGCGATCC AGCGGACCTA	840
CGGCTTTTC GAGCTTCAGC CCGGCGGCG CCGTCACTG CCGGAGCGG TCGCGGGTCT	900
GTTCGGCTTC ACTCGACTAT TAAAGCGCA CCGGGGGGGA CGAGTGGTCT TCGCGGGGGC	960
GGGGCGGGT CTGGCGGGC GTTCGGGGT CCGGCGGGC GTGCGCGGA AGAGTCAGCA	1020
GGGTGTCAGC AAGCGCGGC GAGCTCTGTC CGGAATTC	1058

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (a) LENGTH: 327 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGACA GACCGATGTC GTACCGCTCG CCGAGGAGCC AGTAATTTT GACCGATCT	60
CGGCGAGCT GAAAGCCGAG ATCGACGAGG TGAATCGAC GCGAGTTTC TTGAGGGCC	120
AGTGGCGTGG CCGGGGAGG ACCGCGGGC AGGCGGCTT GGTGCGCTTC CAAGAGGAG	180
CCATATGACA GAGGAGGAA CTCGAGGAGA TCTGAGGAA TATTCGTG GCGGCGCTTC	240
AATACTCGAG GCGCGAGGAG GAGCAGGAGC AGGCGCTTC CTCGAGGAG GGTTCGTG	300
CGGTAATAC GAAAGAGAA GCGGCGA	327

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (a) LENGTH: 170 base pairs
- (b) TYPE: nucleic acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTCCGAGAT	GATGGGCTTG	TCGAGATGTA	CGATCTCTGT	ACCGCGCTGG	TTGAGATGTA	60
CGACACACGT	GTGAGCGTGG	GCAATGTGAG	CGACCGCGTG	GATCTCGGTG	ATCTTGTCTC	120
TCTTCATGAG	GAGATGACAA	CGCGGACAGG	TGACCTCGAG	TACCTTTGAG		170

## (2) INFORMATION FOR SEQ ID NO:48:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG	CATGGGGGGT	GCGGGGGGCA	GCACCGCTGG	CGTGGCGGAG	AATGGGGGGG	60
CGGGGGGTGG	CGCGCGAAGC	GGTGGGGTGC	TCCTCGGCAA	CGGCGGTGCC	GGGGGGACG	120
GGGCGGT						127

## (2) INFORMATION FOR SEQ ID NO:49:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGCGAAG	GGGGGGGCG	CGCGGACCG	GAGGGGGGCG	CGGCGCGCA	AGCGCGCAA	60
CGGCGGTCC	GGCGAAGC	G				81

## (2) INFORMATION FOR SEQ ID NO:50:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGCT	CGCGGCTCC	GGCGAAGG	CGGGTAAGG	AGGAGCTGC	GGATGTTG	60
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GCACGCGHCG HGGCGGGNGAT GCGGCGCGCT CCGACCGNMG CGGTGACGSC GCGGCCGCG 120

GAAACGGTGG TCGCGGTGG CTGATCTG 149

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGACGAGA TCACCTTAC CGGTGATG AGATCGTGG GAGTCGCGG GAGGGTCTG 60  
 ACCCGGMAI CCAGGGGAT CTGGCGCGAG CTGGCGMAG CATGCGGCG CTGCGCTGGT 120  
 TCGAATACA GTCAATTCG GCGCACCTG TCGACGAGG GGTGCGGAC TTGCGAGTGA 180  
 CTATGAGAT CGCTTCCCG CTGGAGGATT CCGAAGCTT CAAGCGCGG CGTAACTGA 240  
 GGTGCATGAT TAAGGACTT TTGCGAACA TCGTGACGG CTCGAGAGC GGTTCAGCGG 300  
 ACGTGCGTC CCGCGAGCG CTGCTCGAA ATCGCTGGG ACAATTGTC GCGG 355

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 999 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCTATCG ATACCATCA CATGATCAG GTGGAGCGGA ACTTGACAG TCGGAGGGA 60  
 CGATTGCGG CACTGGGTAT GCGGCGGATG GCGAGCGCCA GCTGTGTAC GGTTCGCTG 120  
 CGCGGACCG CGAGGCGCA TCGGAGGCG GCGCGCGCG TACCGAGAG GCGGCGCTCG 180  
 CGCGGCTGA CGCTGCGC GCGACGCGA CGCGGACAC CTGTGCGCG CGGACGACCG 240  
 GCGGCGCCA ACACCGGAA TCGGAGCGG GCGGATCGA AGCGAGTAC TCGCGCGCG 300  
 GCGCGGAGG GAGCGCGCT ACTGTGATT GCGGAGAGC CAGCGGACG TGTGCGGAT 360  
 GCGACCGCG TTGAGGATT CAGCTTGGG CTGCTGCTG GCTGCGTGA GTTCGACCG 420  
 GCGGCTTGG ACTAGGTTG AGCACTCTG AGCAAGGCA CTGCGGAGCG GCAATTTCG 480  
 GCGAGCGCG GCGGCGTGG CATGACACG CGTATGTCG TCGGCGGCTG AGAGGAGAG 540



```

CTTACGCCA GCGCGAAGC CACCGATCC AAGCGCGGG CCGGCTTGG CTGGAGATG 600
CGTAGTTCT ATATGCTTA CCGCGGACG CGGATCACC AGGAGACCT CTGCTCCAC 650
CGCAACGGG TGTCTGAAG CGCTCGTAT TAGCAAGTC AGTTCAGCA TCGAGTAG 720
CGGACGGCC AGATCTGAC GGGCGTATC GGTCTCCCG CGCGGACCG ACGGACGCC 780
GGGCTCTTC AGCGTGGT TGTGTTATG CTGCGGAGC CAAACACCC GGTGACAA 840
GGCGCGCCA AGCGCTTCC GGAATCGAT CCGCTTTGC TCGCCCGCC GCGCGCGCC 900
GCACCGGTC CTGCGAGAC CGCTCGGGG CCGCGCGCG CGCGGAGT CGCTCTACC 960
CGGACGACG CGACACGCC CGGACCTTA CCGGCTGA 990

```

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
- (a) LENGTH: 332 amino acids
- (b) TYPE: amino acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1          5          10          15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20          25          30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35          40          45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50          55          60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65          70          75          80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85          90          95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100         105         110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115         120         125

Phe Ala Leu Pro Ala Gly Trp Val Gln Ser Asp Ala Ala His Phe Asp
130         135         140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145         150         155         160

Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165         170         175

```

```

Leu Asp Gln Lys Leu Tyr Ala Ser Ala Gln Ala Thr Asp Ser Lys Ala
    180                               185                               190
Ala Ala Arg Leu Gly Ser Asp Met Gly Gln Phe Tyr Met Pro Tyr Pro
    195                               200                               205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
    210                               215                               220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
    225                               230                               235                               240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
    245                               250                               255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
    260                               265                               270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Gln
    275                               280                               285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
    290                               295                               300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Gln Val Ala Pro Thr
    305                               310                               315                               320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
    325                               330

```

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Arg Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val
1                               5                               10                               15
Val Ala Ala Leu
20

```

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys  
1 5 10 15  
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Glu Pro Phe Asp Pro Ala Trp Gly Pro  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Glu Glu Asa Ala Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro  
 1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser  
 1 5 10 15  
 Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:63:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xii) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Gln Arg Lys  
 1 5 10 15  
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala  
 20 25 30  
 Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala  
 35 40 45  
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro  
 50 55 60  
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln  
 65 70 75 80  
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala  
 85 90 95  
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg  
 100 105 110  
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Gln His Gly Asp Leu Pro  
 115 120 125  
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala  
 130 135 140  
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr  
 145 150 155 160  
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala  
 165 170 175  
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Asn  
 180 185

## (2) INFORMATION FOR SEQ ID NO:64:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 148 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1             5             10             15

Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
20             25             30

Gly Val Gln Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
35             40             45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
50             55             60

Ala Gly Arg His Pro Asp Ser Arg Ile Phe Leu Asp Asp Val Thr Val
65             70             75             80

Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
85             90             95

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
100            105            110

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
115            120            125

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
130            135            140

Thr Gly Gly Pro
145

```

## (2) INFORMATION FOR SEQ ID NO:65:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
 1             5             10             15

Gly Pro Asp Arg Ser His Ser Leu Ser Leu Val Arg His Arg Arg Gln
20             25             30

```

```

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
  35                               45
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
  50                               60
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
  65                               75                               80
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Gln
  85                               90                               95
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
 100                               105                               110
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
 115                               120                               125
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
 130                               135                               140
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
 145                               150                               160
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
 165                               170                               175
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
 180                               185                               190
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
 195                               200                               205
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
 210                               215                               220
Phe Pro Ile Val Ala Arg
 225                               230

```

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (a) LENGTH: 132 amino acids
  - (b) TYPE: amino acid
  - (c) STRANDEDNESS: single
  - (d) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20           25           30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35           40           45

```

```

Leu Gly Val Val Asp Ser Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50                      55                      60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65                      70                      75                      80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85                      90                      95
Asp Ala Leu Asn Gly Ala Ala Pro Gly Asp Val Ile Ser Val Asn Trp
100                     105                     110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gln
115                     120                     125
Gly Pro Pro Ala
130

```

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1      5      10      15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Leu Ser Asn Pro Pro
20      25      30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35      40      45
Met Ala Arg Val Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50      55      60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65      70      75      80
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85      90      95
Ser Gln Arg Lys
100

```

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1      5      10
Leu Tor Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20     25     30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35     40     45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50     55     60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65     70     75     80
Thr Ala Val Gly Gly His Asp Glu Ala Gly Asp Arg Arg Asp Gln Arg
85     90     95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100    105    110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115    120    125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130    135    140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145    150    155    160
Asp Arg Arg

```

## (12) INFORMATION FOR SEQ ID NO:69:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1      5      10
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20     25     30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35     40     45

```

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro  
 50 55 60  
 Arg Gly Arg Lys Gln Ala Val Ala Ala Val Ala Ala Ser Leu Arg  
 65 70 75 80  
 Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly  
 85 90 95  
 Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Val Gly Thr Ala Pro Ala Ala  
 100 105 110  
 Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr  
 115 120 125  
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Gln Tyr  
 130 135 140  
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val  
 145 150 155 160  
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu  
 165 170 175  
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu  
 180 185 190  
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro  
 195 200 205  
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe  
 210 215 220  
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro  
 225 230 235 240  
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro  
 245 250 255  
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro  
 260 265 270  
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala  
 275 280 285  
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu  
 290 295 300  
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr  
 305 310 315 320  
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Gln Gly Gln  
 325 330 335  
 Val Ser Arg Gln Asn Pro Thr Gly  
 340

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1          5          10          15
Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20          25          30
Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35          40          45
Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50          55          60
Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65          70          75          80
Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85          90          95
Thr Gly Gln Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
100          105          110
Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
115          120          125
Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
130          135          140
Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
145          150          155          160
Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala His
165          170          175
Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
180          185          190
Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
195          200          205
Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
210          215          220
Met Gly Gly Arg Arg Arg Gly Ala Cys Met His Val Leu Asp Val Ser
225          230          235          240
His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
245          250          255
Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
260          265          270
Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
275          280          285

```

Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile  
 290 295 300  
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp  
 305 310 315  
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala  
 320 325 330 335  
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn  
 340 345 350  
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp  
 355 360 365  
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp  
 370 375 380  
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala  
 385 390 395 400  
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu  
 405 410 415  
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg  
 420 425 430  
 Leu Ala Thr Arg Leu Met Arg Arg Ile Glu Glu Ala Ala His Thr Ala  
 435 440 445  
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp  
 450 455 460  
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Glu Val Thr Ser  
 465 470 475 480  
 Val Ala Pro Thr Gly  
 485

## (7) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu  
 1 5 10 15  
 Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val  
 20 25 30  
 Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala  
 35 40 45

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His  
 50 55 60  
 Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu  
 65 70 75 80  
 Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Gln Thr Pro  
 85 90 95  
 Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Gln Gly Asp  
 100 105 110  
 Asp Cys Pro Asp Ser Thr Asn Ala Val Lys Gly Leu Thr Asn Ala Pro  
 115 120 125  
 Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn  
 130 135 140  
 Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala  
 145 150 155 160  
 Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Tyr Ser Asn Leu Asp  
 165 170 175  
 Cys Ala Pro Ser Asn Gln Thr Leu Val Lys Thr Phe Ser Pro Gly Glu  
 180 185 190  
 Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg  
 195 200 205  
 Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val  
 210 215 220  
 Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn  
 225 230 235 240  
 Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln  
 245 250 255  
 Ala Pro Pro Pro Gln Ser Pro Ala Gln Gly Gly  
 260 265

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val  
 1 5 10 15  
 Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Gln Val Val Ala  
 20 25 30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr  
 35 40 45  
 Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala  
 50 55 60  
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp  
 65 70 75 80  
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu  
 85 90 95  
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 364 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala  
 1 5 10 15  
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser  
 20 25 30  
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser  
 35 40 45  
 Thr Ala Gln Gln Asn Ala Met Gln Gln Pro Val Tyr Ala Tyr Val Arg  
 50 55 60  
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn His Asn Gly Ser Gly Ala  
 65 70 75 80  
 Gly Val Thr Gln Phe Leu Asn Asp Gln Thr Asp Phe Ala Gly Ser Asp  
 85 90 95  
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Gln Arg  
 100 105 110  
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala  
 115 120 125  
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro  
 130 135 140  
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro  
 145 150 155 160  
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asn Leu Pro Pro Thr Pro Ile  
 165 170 175

```

Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
180                               185                               190

Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
195                               200                               205

Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
210                               215                               220

Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
225                               230                               235

Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
240                               245                               250                               255

Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
260                               265                               270

Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Arg Leu Val Leu
275                               280                               285

Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile
290                               295                               300

Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
305                               310                               315                               320

Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
325                               330                               335

Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
340                               345                               350

Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
355                               360

```

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Arg
1      5      10      15

Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
20     25     30

Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
35     40     45

Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
50     55     60

```

Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg  
 65 70 75 80  
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro  
 85 90 95  
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg  
 100 105 110  
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp  
 115 120 125  
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val  
 130 135 140  
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg  
 145 150 155 160  
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly  
 165 170 175  
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala  
 180 185 190  
 Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val  
 195 200 205  
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro His Arg Arg Ser Arg  
 210 215 220  
 Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro  
 225 230 235 240  
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg  
 245 250 255  
 Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His  
 260 265 270  
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr  
 275 280 285  
 Ala Gly Val His His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg  
 290 295 300  
 Asn Arg Pro Arg Arg  
 305

## (2) INFORMATION FOR SEQ ID NO:75:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 580 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (X1) SEQUENCE DESCRIPTION: SEQ ID NO:75:



Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly  
 1 5 10 15  
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys  
 20 25 30  
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala  
 35 40 45  
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys  
 50 55 60  
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr  
 65 70 75 80  
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser  
 85 90 95  
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His  
 100 105 110  
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln  
 115 120 125  
 Gln Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro  
 130 135 140  
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr  
 145 150 155 160  
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Phe Pro Ser Pro Pro Pro Gln  
 165 170 175 180  
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro  
 185 190  
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Phe Pro Pro Gly Met  
 195 200 205  
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr  
 210 215 220  
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val  
 225 230 235 240  
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala  
 245 250 255  
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val  
 260 265 270  
 Gln Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr  
 275 280 285  
 Asp Leu Gly Arg Gln Ser Glu Gln Gly Ser Gly Phe Ile Leu Ser Ala  
 290 295 300  
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys  
 305 310 315 320  
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp

	325		330		335
Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp	340		345		350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser	355		360		365
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile	370		375		380
Gly Ser Pro Leu Gly Leu Gln Gly Thr Val Thr Thr Gly Ile Val Ser	385		390		395
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Gln Ala Gly Asn Gln Asn	405		410		415
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asp	425		430		435
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn	445		450		455
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly	465		470		475
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile	485		490		495
Ala Asp Gln Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly	505		510		515
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Gln	525		530		535
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val	545		550		555
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu	565		570		575
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr	585		590		595
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly	605		610		615
Lys Ala Gln Gln	620				

(2) INFORMATION FOR SEQ ID NO:76:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1      5      10
Gly Ala Cys Iasn Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
20     25     30
Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
35     40     45
Ala Leu Leu Ala Glu Ile Arg Glu Ser Leu Asp Ala Thr Lys Gly Leu
50     55     60
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu
65     70     75     80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala
85     90     95
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg
100    105    110
Val Glu Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
115    120
Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
130    135    140
Ala Gly Val Thr Glu Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
145    150    155    160
Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
165    170    175
Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
180    185    190
Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
195    200    205
Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
210    215    220
Lys Trp Asn Glu Pro Val Asn Val Asp
225    230

```

(x) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala

110

1	5	10	15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val			
20	25	30	
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile			
35	40	45	
Thr Tyr Arg Ile Lys Leu Gln Val Ser Phe Lys Met Arg Pro Ala Gln			
50	55	60	
Pro Arg			
65			

## (12) INFORMATION FOR SEQ ID NO:78:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser		
1	5	10
Cys Ala Ser Pro Pro Ser Phe Phe Leu Pro Pro Ala Pro Pro Val Ala		
25	30	35
Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro		
40	45	50
Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro		
55	60	65
Ser Pro Pro Leu Pro		
65		

## (12) INFORMATION FOR SEQ ID NO:79:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser		
1	5	10
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala		
20	25	30

## III

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu  
 35 40 45  
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val  
 50 55 60  
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr  
 65 70 75 80  
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val  
 85 90 95  
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln  
 100 105 110  
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala  
 115 120 125  
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly  
 130 135 140  
 Gly Gly Val Ala Val Gly Gln Pro Val Val Ala Met Gly Asn Ser Gly  
 145 150 155 160  
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu  
 165 170 175  
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Gln Thr  
 180 185 190  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
 195 200 205  
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr  
 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
 225 230 235 240  
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly  
 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val  
 275 280 285  
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
 290 295 300  
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp  
 305 310 315 320  
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Tyr Gln  
 325 330 335  
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gly Gly  
 340 345 350  
 Pro Pro Ala

355

## (2) INFORMATION FOR SEQ ID NO:80:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Ser Pro Lys Pro Asp Ala Glu Gln Gln Gly Val Pro Val Ser Pro Thr
 1             5             10
Ala Ser Asp Pro Ala Leu Leu Ala Gln Ile Arg Gln Ser Leu Asp Ala
 20            25
Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
 35            40            45
Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
 50            55            60
Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
 65            70            75            80
Val Pro Phe Arg Val Gln Gly Asp Asn Thr Ser Val Lys Leu Phe Asp
 85            90            95
Asp Trp Ser Asn Leu Gly Ser Ile Ser Gln Leu Ser Thr Ser Arg Val
100           105           110
Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
115           120           125
Leu Gln Ala Gln Gly Thr Gln Val Ile Asp Gly Ile Ser Thr Thr Lys
130           135           140
Ile Thr Gly Thr His Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
145           150           155           160
Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
165           170           175
His His Leu Val Arg Ala Ser His Asp Leu Gly Ser Gly Ser Ile Gln
180           185           190
Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
195           200           205

```

## (2) INFORMATION FOR SEQ ID NO:81:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val  
 1 5 10 15  
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln  
 20 25 30  
 His Ala Asp Gly His Ser Leu Leu Asp Ala Thr Asn Pro Ala Val  
 35 40 45  
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu His Gly Tyr Ile Xaa Glu  
 50 55 60  
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe  
 65 70 75 80  
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Glu Pro Pro Glu Pro Glu  
 85 90 95  
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala  
 100 105 110  
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val  
 115 120 125  
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala His Glu Trp  
 130 135 140  
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn  
 145 150 155 160  
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg  
 165 170 175  
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly  
 180 185 190  
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Glu Ile  
 195 200 205  
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe  
 210 215 220  
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp  
 225 230 235 240  
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg  
 245 250 255  
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln  
 260 265 270  
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys  
 275 280 285

## (12) INFORMATION FOR SEQ ID NO:52:

## (4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (8) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1             5             10             15
Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20             25             30
Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg
 35             40             45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
 50             55             60
Val Glu Ile Pro Gly Val Asp Tor Val Arg Asn Gln Phe Asp Arg Pro
 65             70             75             80
Arg Gln Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
 85             90             95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Gln Gly Asp Phe Leu
100             105             110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Glu Ile Glu Glu Val
115             120             125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
130             135             140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
145             150             155             160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
165             170

```

## (2) INFORMATION FOR SEQ ID NO:83:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (8) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
 1             5             10             15

```



Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly  
 20 25 30  
 Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro  
 35 40 45  
 Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa  
 50 55 60  
 Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp  
 65 70 75 80  
 Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Gln Gly Gly Ile  
 85 90 95  
 Gly Gly Xaa Gln Gly Xaa Xaa Arg Arg Xaa Gln  
 100 105

## (7) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn  
 1 5 10 15  
 Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr  
 20 25 30  
 Arg Arg Ala Leu Gln Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly  
 35 40 45  
 Val Lys Gln Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr  
 50 55 60  
 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr  
 65 70 75 80  
 Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Gln  
 85 90 95  
 Gln Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr  
 100 105 110  
 Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
 1           5           10           15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
 20           25           30
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
 35           40           45
Ala Asp Leu Ala Gln Ile Lys Ala Gly Gln Ser Val Leu Ile His Ala
 50           55           60
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
 65           70           75           80
Gly Val Gln Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
 85           90           95
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
100           105           110
Arg Ser Ser Xaa Gly
115

```

(x) INFORMATION FOR SEQ 70 NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
 1           5           10           15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
 20           25           30
Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
 35           40           45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50           55           60
His Arg Asp Met Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65           70           75           80
Ile Leu Gln Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
 85           90           95

```

85  
Pro Ala Ala Gly Gly Gly Ala  
100

## (2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Glu Trp Arg Gly Met Leu Gly  
1 5 10 15  
Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His  
20 25 30  
Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala  
35 40 45  
Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly  
50 55 60  
Gly Arg Leu Val Val Glu Leu Thr Pro Arg Glu Ala Ala Ala Leu Gly  
65 70 75 80  
Asp Glu Leu Lys Gly Val Thr Ser  
85

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile  
1 5 10 15  
Ser Gly Asp Leu Lys Thr Cln Ile Asp Gln Val Glu Ser Thr Ala Gly  
20 25 30  
Ser Leu Glu Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Glu Ala  
35 40 45  
Ala Val Val Arg Phe Gln Glu Ala Ala Asp Lys Gln Lys Gln Glu Leu  
50 55 60

Asp Glu Ile Ser Thr Asn His Arg Gln Ala Gly Val Glu Tyr Ser Arg  
 65 70 75 80  
 Ala Asp Glu Gln Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO:89:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Thr Gln Ser Glu Thr Val Thr Val Asp Gln Gln Glu His Leu Asn  
 1 5 10 15  
 Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val  
 20 25 30  
 Pro His Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln  
 35 40 45  
 Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala  
 50 55 60  
 Lys Glu Arg Glu Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa  
 65 70 75 80  
 Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly  
 85 90 95  
 Glu Gly Thr Val Glu Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser  
 100 105 110  
 Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro  
 115 120 125  
 Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp  
 130 135 140  
 Glu Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr  
 145 150 155 160  
 Leu Thr Leu Glu Gly Asp  
 165

## (2) INFORMATION FOR SEQ ID NO:90:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Ala Glu Arg Met  
1 3

## (2) INFORMATION FOR SEQ ID NO:91:

## (1) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 263 amino acids
- (b) TYPE: amino acid
- (c) STRANDEDNESS: single
- (d) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Trp Met Ser Val Thr Ala Gly Glu Ala Glu Leu Thr Ala Ala  
1 5 10 15  
Glu Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr  
20 25 30  
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu  
35 40 45  
Ile Ala Thr Asn Leu Leu Gly Glu Asn Thr Pro Ala Ile Ala Val Asn  
50 55 60  
Glu Ala Glu Tyr Gly Glu Nor Trp Ala Glu Asp Ala Ala Met Phe  
65 70 75 80  
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe  
85 90 95  
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Glu Ala  
100 105  
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Glu Leu Met  
110 115 120 125  
Asn Asn Val Pro Glu Ala Leu Lys Glu Leu Ala Glu Pro Thr Glu Gly  
130 135 140  
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro  
145 150 155 160  
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn Ala Met  
165 170 175  
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met  
180 185 190  
Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Glu Ala Val Glu Thr Ala  
195 200 205

120

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly  
 210 215

Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala  
 225 230 235 240

Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Asn Ser Gly  
 245 250 255

Arg Arg Asn Gly Gly Pro Ala  
 260

## (2) INFORMATION FOR SEQ ID NO:92:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (3) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala  
 1 5 10 15

Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Gln Gly  
 20 25 30

Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly  
 35 40 45

Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr  
 50 55 60

Gln Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro  
 65 70 75 80

Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val  
 85 90 95

Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu  
 100 105 110

Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr  
 115 120 125

Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln  
 130 135 140

Ala Val Ala Ala Val Leu Ala Leu Leu Val Gln Thr Gly Ala Ile Thr  
 145 150 155 160

Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg  
 165 170 175

Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly  
 180 185 190

(21)

Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Glu Ser Pro Gly Pro Gln  
 195 200

Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser  
 210 215 220

Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala  
 225 230 235 240

Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser  
 245 250 255

Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser  
 260 265 270

Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn  
 275 280 285

Pro Ser Gly Gly Gln Gln Ser Ser Ser Pro Gly Gly Ala Pro Val  
 290 295 300

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Gln Ala Gly Asn  
 1 5 10 15

Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile  
 20 25

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Tyr Arg Gly  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

122

(A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala  
 1 5 10 15  
 Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu  
 1 5 10 15  
 Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu  
 20 25

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr  
 1 5 10 15  
 Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid



125

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(\*1) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu
1			5					10						15	
Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe				
			20					25							

(2) INFORMATION FOR SEQ ID NO:98:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 507 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(\*1) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG TGAATAGGAT GGCGCGAGAT CTGACCGCGC CGGCTGCAT CCGCCGCGCT	60
CGCGCGCGTG TGACTTCGAT CATCGCTGCG GCGCGGCTCG TATACCGAGT GCGGCGCGTC	120
GTCTTGGGCG CGGCACTGCG GTTGGACCGG GCATCGCGCG CTGACCTTCG GACGCGCGCG	180
CAGTTGACCA GCGTCTCTCA CAGCGTGGCG GATCGCGAGG TGTCTTTTGC GAACAGCGGC	240
ATTCTGCTCG AGGCGCGCAT CGGCGCGACC GAGGCGCGCA TCGCGACCA CAGCTGAAG	300
AAGCGCGCGC ACCATCGGGA TCTCGCGCTG TCGTTCGCGG TCAGCGAGAT CGAGCGCGCG	360
GCGCGCGGTT CGGCGACGCG CGAGCTTCG GTCTCGCGTG CGAGCTTCG GTCGCGCGTG	420
ACCGAGAGCG TCAGCTTCGT GAATCAAGCG CGCTGATGTC TGTACGCGCG ATCGCGCGATG	480
GAGTTCTTGC AGGCGCGCGG CAGCTGA	507

(2) INFORMATION FOR SEQ ID NO:100:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(\*1) SEQUENCE DESCRIPTION: SEQ ID NO:100:

124

```

Met Lys Met Val Lys Ser Ala Ala Ala Gly Leu Thr Ala Ala Ala Ala
1      5      10
Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
20     25     30
Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
35     40     45
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
50     55     60
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
65     70     75     80
Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Gln Ala Arg Ile Ala Asp
85     90     95
His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
100    105    110    115
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
120    125    130
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
135    140    145
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
150    155    160
Glu Leu Leu Gln Ala Ala Gly Asn
165

```

## (2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 506 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

CGTCGCAATG TCGTTGACCG TCGGGGCGCG CGTCGCGCTC CGCATGTGCG TCGACGCGCT      40
CATTACACCG ACTTCGAATT AGGGGCGAGCT AGTAGCTGCG CTCACGCGGA CGGATCGCGG      80
GGCTCGCGCA GAGTTGACCG CTTCACCGGT GGGCGAGTCC TATTGCGGGA ATTTCGTGCG      120
CGCACGCGCG GGTTCGCGCG CTGCGATGCG CGCGCATTCG CAGGCTGTGC GGGGGGCGGC      160
ACGATACATC AGGCTGTGCG AGTCGCTTTC CGGCTGCTGC AACCACTATT AAGCGGTGCG      200
GGGGGCGCAT CGCGGACGCG GCGTGTGCGC CGGGGCTAGG CGGATGTGCG CGGCTGTGCG      240
AGCGGCGCGA TCGCGGACCG CGGCGATGCG GCGGGGCGTA GCGGAGATTG GCGGCTGTCT      280
CGAGCGCGCG CATCTGCTGC CGAATGCTG GAGCGCGCGG GATCGGCTAG TCTGAGAGCG      320

```

GCGGTCACCG CCGTGGAGCT

505

127 INFORMATION FOR GEO ID NO: 102:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1				5					10					15	
Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala
			20					25					30		
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
			35				40					45			
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Phe
			50			55					60				
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
			65			70				75					80
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr
			85					90					95		

## (2) INFORMATION FOR DEC ID NO:163.

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (1x) SEQUENCE DESCRIPTION: 800 TO 899, 103.

ATGAGAGGAC	AGCACTGGAA	TTCCGCGGGT	ATCAGAGCGG	GCGCAAGCGC	AATCCAGGGA	60
AATATCAGCT	GCATTTATTC	CTCTCTTGAC	GAGGGGAAGC	AGTCCCTGAC	CAGCTCTCGA	120
GCGGCTGAGG	GCCTTAGCGG	TTCCGAAGCG	TACC			154

## (2) INFORMATION FOR SEQ ID NO:104:

## (4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1             5             10             15
Ala Ile Gln Gly Asn Val Thr Ser Ile Ala Ser Leu Leu Asp Glu Gly
 20             25             30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser
 35             40             45
Gln Ala Tyr
 50

```

## (2) INFORMATION FOR SEQ ID NO:105:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

CGCTCCGCGCA CTTCACAGTC ACTATGAAGC TCGGCTTGGC NCTGAGGAT TCTCGAGCTT      60
TCAGGCGCGG CGGATAACTG AGGTGCAATC TTAAAGGACT TTTCAGAAAC ATGCTTACGC      120
GCTCGAAAGC CGGCACAGCC GAGCGTGGCT CGGCGAGGAC GTTCGCTCCA AATGCTCTGA      180
GAGCAATTCG CGGCGGCGCC TACAGGAGAG TCGGTCTGTA ATTGCGCGAG TATCTGGTGG      240
ACCTGHTTGG TCTGAGCGG GAGCAAGCGG TCTCTACGCT CG
282

```

## (2) INFORMATION FOR SEQ ID NO:106:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3058 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

GATGATAGCG GTGCAAGTGC TCGGCGGCTT TCGGAGTGGC GTGCAAGTGC CTTTGATGAT      60
GGGATACCCA GAGATGTTCG CGGCGGCGCG TCACACCGTG CAGAGCAATC GTCTTACCAC      120
TCTGCTTAGC AATGCGGCTG CGGCGGCGCG GAGGACTGGG GTGCTGCGCG CGGCTGCGCA      180

```

TCAGGTGTCG	GCCTGCACTG	GAGGSCACTT	CGGCGACATF	CGCGGATGT	ATCAGTGGT	240
GAGGGTCGG	GCTGTGGA	TTGATGACA	GTTCGTGGC	ATCCTTGCA	GCAGCGGAG	300
CTGTATGCG	GACACTGAG	TGGCAATGC	GCGGGGGCC	AGCTTAGCA	GGACAGTCC	360
GCACGAGAA	CCACGAGAA	TAGGACACG	TAATGTTGA	TTGCGGGCC	TTACGACGG	420
AGATCAACTC	CGCGAGATC	TACCGTGGC	GGGTTGGC	GTGGTGGG	GCAGCGCTC	480
AGATGTGGA	CAGCTGGCG	ACTGAGCTG	TTTGGGGCC	GTGCGGTTT	CAGTGGTGG	540
TGTGGGTTT	GACGTGGGG	TGTPGATAG	GTTCGTGGC	GGTCTGAG	GTGGGGCGG	600
CTTGGCGTA	TGTGGGTGG	ATGAGGCTA	CGCGGGACA	GCAGGAGTG	ACGCGCGCC	660
AGGTGGGTT	TGTTGGGGC	GCTTACAGA	CGGTGATGG	GCTGAGGGT	CGCGGGCGG	720
TGATCGCGA	GACCGTGGT	GAACTGATG	TTCTGATGG	GACCAAGCT	TTGGGGGAAA	780
ACACCGGCG	GATCGGGTC	AACGAGGCG	ATACGGGA	GATGTGGG	CAAGCGCGG	840
CGGAGATTT	TGGTACGCG	GCGGGGACG	CGAGGGGCG	GGGAGGTTT	CTGGCGTTG	900
AGGAGGCGG	GGAGTGGG	ACCGGGGGT	GGTCTGGA	GCAGGGCGG	GGGTGGAGG	960
AGGCGTGGG	CAGCGGGCG	GGGACGAGT	TGATGAGAG	TGTGGCGCG	GGGTGGGAG	1020
AGGTGGGCA	GGGAGGGAG	GGGACGAGC	CTTCTTCAA	GCTGGGTGG	CTGTGGAGG	1080
CGGTCTGGC	GCATGGGTG	GGATCGGCA	ACATGGTGG	GATGGCGAG	AACGACATG	1140
CGATCGGCA	CTGGGTGGT	TGATGAGCA	ACAGCTTGG	CTGATGTTG	AGGGGCTTG	1200
CTGGAGGGG	GGGCGGAG	GGGTGCGAA	CGGCGGCA	AAAGGGGCT	CGGGGAGAG	1260
GCTCGGTGG	CAGCTGGGT	GTTCTTGGG	GTTGGGGG	TGGGGTGGG	GGCAAGTTG	1320
CTCGGGGCG	CTGGGTGGT	TCCTTGGG	TGCGGGGCG	CTGGGGGGG	GGCAAGGAG	1380
CAGTCAAGC	GGGGGGGCG	GGGTGGGCG	TGAGGAGCT	GAGGAGGCG	GGGAGAGAG	1440
GGCGGGGGA	GATGTGGGG	GGGTGGGCG	TGGGGGAGT	GGGGGGGAG	GGGTGGGTT	1500
GGCTAGTGG	TGTGTGGGT	GTTCGGGGC	GAGGAGGCT	GATGGGGAT	TCTGTGGGG	1560
GGGGTAGGA	GAGGGGGCG	AGACTGTGGT	TATTTGAGC	GTGATGGGG	GTTCGGGCT	1620
TTCTGGGCG	GGTATGAGC	ACATGGAAT	TGATGAGCA	GTGAGGTTA	TTAGGTGCA	1680
GTTCAGAGG	GAGAGAGG	ACATGGGCT	AGTTTTATG	ACGATGGCG	AGGATGGCG	1740
GGATATGGC	GGCGTTTTG	AGGTGAGCG	CGAGGAGTG	GAGGAGGAG	GTTCGGGAT	1800
GTGGGGTGG	GGGAGAGCA	TTTGGGTGG	GGGTGGAGT	GGATGGGG	AGGAGGCTC	1860
GCTAGACCG	ATGGGGGAG	TGATCAGGG	GTTCGGGAG	ATGGGAGCA	TGCTGAGCG	1920
GTGGGTGGC	GGGTGGGTT	GGGAGGCA	CACTAGGAG	GAGGAGGAG	AGGCTTGGC	1980
GCGATGCTC	AGGAGTGGC	GTGGGTGGT	GGGAGGAGT	ACTTTTACAA	GGGAGGAGG	2040

```

ACAGTTTCCA TGACUATCAA CTATCAATTC GGGGATGCG AGGCTCAGG CGCATGATC 2100
CGCGTCAAG CGGRTTCTT GAGGCGCGAG CATCAGGCCA TTATTCTGTA TGTCTTGACC 2160
GCGATGACT TTGGGGCGG CGCGGCTTC GCGGCTGCG AGGCTTCAT TACCCAGTTG 2220
GGGCTACTT TCGAGTGAT CTACAGACAG GCGAAGCGC ACGGGCAGAA CGTCGAGGCT 2280
GCGGCGACG ACATGACGCA AACCGACGC GGGTCTGGT CCAGCTGCG CTGACACAG 2340
GCGAGGCCA GAGAGCTGT GTACGAGTGA AATTCTCTGC GTGATCTTC GCGTGGCAGT 2400
CTAAGTGGTC AGTCTGCGG TCTTGCTGT TTGCTCTTG GCGGCTTCTT CGTCTCTGCT 2460
CAGTCTCTT CGGCTGCGG TGAGGCGCT GAGGCGCGG TAGCGCGCT CTTCGATCT 2520
TTCTCTCTT TCTTCTGCG GAGGCGCTC GAGGCGCGC ATGATCGAG CGCGTCTGCG 2580
GAGATGCTT ACATCTCTG TTGCGCTCT TACTCTCTG TTGAGGCTT CCGTGGCTT 2640
GTGAGCGCG ATTTCGCGC AGATCTCTT GCGGAGCGG GTGAGCGCA GCGGCTCTT 2700
GCGGCGCTT TCGAGCTGT GCGGCGCGC GCGGCTTCT TCGGCTAGG CGTCTGAGT 2760
CGCATCATAT TGGGCAACA CTGATCTCT GTGCGCTCT TCGGCTAGG AGTCTGAGG 2820
GCTGCGCTT CAGGCGCGG AGGCTCTCT GCTGCTCTT ATCAGATTC CTGCTCTCT 2880
GCTCTCTCT CAGTCTCTG GCGTCTCTG CAGGCTCTT CCGATCTCT CAGGCGCGC 2940
GCGTCTCTT TCGCTCTG CAGGCGCGC GCGGCGCGC GCGGCGCGC GCGGCTCTT 3000
GAGAGCGCG AGGCTCTCT GCGGCTCTT GCGGCGCGC AGGCTCTCT CAGGCTCT 3058

```

## (2) INFORMATION FOR SEQ ID NO:107:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (a) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1      5      10      15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Glu Met Trp
20     25     30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Glu Ser
35     40     45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
50     55     60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr

```

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65	70	75	80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Glu Val Arg Val Ala Ala Ala	85	90	95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala	100	105	110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly	115	120	125
Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met	130	135	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala	145	150	155
Thr Ala Thr Ala Thr Leu Leu Pro Phe Gln Glu Ala Pro Gln Met Thr	160	165	170
Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser	175	180	185
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu	190	195	200
Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu	205	210	215
Gly Gly Leu Trp Lys Thr Val Ser Pro Ala Arg Ser Pro Ile Ser Asn	220	225	230
Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val	235	240	245
Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala	250	255	260
Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala	265	270	275
Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly	280	285	290
Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val	295	300	305
Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg	310	315	320
Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly	325	330	335
Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly	340	345	350
Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met	355	360	365
Pro His Ser Pro Ala Ala Gly	370	375	380
385	390		

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1725 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

GACCTCAGCA CCCGCGGTGC AGGCTGGAG CTTGATCGGT TTGAACTCG GTTCAAGGTG      60
AGTTCCTCTG GCTGTCTGCG GCGCTGGATG CAGACTCGAT GCGGTCTTT AGTGCACATA      120
ATTTCGTTGA AGTGCCTTGG AGGTATAGGA CTTACAGATT GGTAAATGTA GGTTCACCCC      180
CTGTTTGGGG TCGATTTCGC CGAGCCAGTC GTACCAACAG CTGGCGTCAC GCGCCAGGCG      240
GGGATCAGA TCGTTTGAAT ACCAATCAAT CTTGAGCTCG CGGCGCGATG CTCGGCTTAA      300
ATGAGGAGGA GCACGCTCT CTTTCACTGC GCAACGGGAG ATGTTGCGGG CCGCGCTCTG      360
CGAATCTGCT TCGCTGGGGG CAGCGCTGGA GGTAGCAAT GCGCGCGCAG CCGTGCCTAC      420
GACTGGGGTG GTGCGCGCGG CTGCGGAGGA GGTGTGCTG CTGCTTGCCA CACAATTCGG      480
TACGCTATGG GCGAGTATTC AGAGCGCCAG CGGCAAGGCC GCGCTGATCC ATGAGCACTT      540
TGTGACCAAG CTGCGCGCGA GCGTATGTT ATATCGGAC ACCGAGGCGG CGAAGCTCTT      600
GCTCACCCTC TAGCTGACCT CAGGCTATTC GCGCGGAGG ATTATCGAG TGTGCAATT      660
TGGGAGGTTA CGAGCGGAGA TCACCTGCG GAGGATGTAC GCGCGCGCGG GTTCCGCTTC      720
GCTGCTGGCC GCGCGGAGGA TGTGGGACAG GGTGGCGAGT GACCTATTTT CCGTCCGCTC      780
GCGCTTTTGA TCGTGTCTCT GCGCTCTGAC GGTGCGGTTC TGATAGCTT CCGCGCGGG      840
TCTGATGCGG GCGCGCGGCT GCGCTTATCT GCGTGGATG AGCTTCACCG CGGCGCGAGC      900
CGAGCTGACG GCGCGCGAGG TCGCGGTTCG TCGCGCGGCG TAGGAGACAG GGTATAGCTT      960
GAGGCTGCGC CGGCTGTGTA TCGCGGAGAA CGGTACGGA CCGATGAGC TGAGTGGAGC      1020
CAACTCTCTG GCGCAAAACA CCGCGCGCAT CGAGGCAAT CAGCGCGGCT ACAGCGAGAT      1080
GTGCGGTGTA GACGCGGAGG GATGTATGCG CTACGCGGCG AGGCGCGGCG CCGCTTCGCA      1140
GCGCTTCTCT CCGTTCTGAG AGCGCGCACT GATGACGAG CCGCGCGGCG TCGTTGAGCA      1200
GCGCTCTGCG GTGAGGAGG CCACTGAGAC GCGCGCGGCG AGCGCTTGA TGAGATATGT      1260
GCGCGAGCGG CTGCAAGCGG TCGCGGAGCG AGCGCGGCG GTGCTGCTCT CTTCGAGCTT      1320
GGTGGGCTG TGAAGCGGCG TCTCGCGGCA TGTGTTGCGG CTGAGAGCG TGAGTTCGAT      1380
AGCGAGAGAG GACATSTGCG TGATGCGGCG GGTGCTGCTG ATGAGGAGCA CTTTGCCTCT      1440

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```

GATTTTGAAG GCGTTAGCTC CGCGGCGCGC TCGAGCGCTG GAAGCCCGCG CGAAARCGG 1500
GCTCTGGGCG ATGAGCTTCC TGGCAGCGCA CGTGGTTCC TGGCTGGGTT CTTCGGGTCT 1560
GGGCGCTGGG GTGGCGGCA ACTTGGCTCG CGCGGCTCC CTGGCTTCTT TGTGGTGGC 1620
GGCAGCATGG GCGCGGCGCA ACCAGCGGCT CAGGCGGCG GCGCGGCGC TGGCGCTGAC 1680
CAGCTGAC AGCGCGGCGC AACCGCGCG CGACACATG CTGGG 1725

```

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Gln Ile Asn Ser Ala Arg Met
 1      5      10
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20     25     30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35     40     45
Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50     55     60
Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65     70     75
Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 80     85     90
Ala Tyr Gln Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
100    105    110
Gln Asn Arg Thr Gln Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
115    120    125
Gln Asn Thr Pro Ala Ile Gln Ala Asn Gln Ala Ala Tyr Ser Gln Met
130    135    140
Trp Gly Gln Asp Ala Gln Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
145    150    155
Thr Ala Thr Gln Ala Leu Leu Pro Phe Gln Arg Ala Pro Leu Ile Thr
160    165    170    175
Asn Pro Gly Gly Leu Leu Gln Gln Ala Val Ala Val Gln Gln Ala Ile
180    185    190
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
195    200    205

```

Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu  
210 215 220

Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn  
225 230 235 240

Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val  
245 250 255

Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala  
260 265 270

Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Trp Ala Met  
275 280 285

Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu  
290 295 300

Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser  
305 310 315 320

Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro  
325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr  
340 345 350

Ala Pro Gly His Met Leu Gly  
355

## (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTCAGTTCG AGCATCATAC TGACGGGACTC TATCCAGGAT GGTGAGACA ACCGAAACCAC 60

GCTCGGAGCG GGGACATATG CAGCCGACG CAGTGGCTT GGGCGCGGAA GCGGAGGCCG 120

CGGAGCGGCA AGCGTTGGCC GCGTCGCGCG GGGCGCGTCC CCGTCGCGCC CGGTTGAGGC 180

GTGAGCGCTT GCGGATGGCT CCGCGGACG AGGAAAGCT CCGGAGGAT ATCGAGACTG 240

GGAGAGGCGC GAGAGCTATC AGGACTATCA TGACTATGAG GCGGAGAGCC AGGAGGCCGC 300

ACGATCGGCA TCTTGGGCAC GCGGCTTGGC GCTCGCGTTA CGAGACTCT CCACGATTGC 360

CATGCGCGCG GCAATCTGCA TCATGTGCGC CTTCACCGGG CTCAGGAGAT ACATTTGTGT 420

GCAACAGCAT GAGGCGAGCG AACGCGACCA GCGCGCGCGC GCTTCGCGCG CGGAGGCCCA 480

GCAAGGTGTC ATCAACATCA CCTCGCTGCA CTTCACGAC GCGAAGAGAG ACGTGGCGCG 540

TGTGATCGAC AGCTCCACCG GCGAATTCAG GGTACTTTC CAGCAGCGCG CAGCCGATTT	600
CACCAAGGTT GTCGAAGAGT CCAAGTGGT GAGXUAGGG AGGTGGAACG CGACAGCUST	660
CGAATCGATG AACGAGCAAT CGGCGDTGGT GCTCGTGGGG GCTACTTCAC GGGTCACCAA	720
TTCCGCTGGG GCGAAGAGCG AACCAAGTGC GTGGCGGGTC AAGTGAACCG TGACCGAAGA	780
GUGGGGACAG TACAGATGT CGAAGTTGA GTTCGTACCG TGACCGATGA CTTACGGGAC	840
GTGAACACCG AAATCTATTG CCGACCGGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCGCGTGATT CCGCGACCGA GGCATTGGAC ACGGACTCTG CAAGCGAATC TACCGCGGAG	960
AAGCGTCAGC GGCACCGTGA CTTCTGGGCA ATCGAGGTTA CATTGAACCC GGTTCGGGTG	1020
ATTCTGATCC TCTCATGTT GATCTCTGGG GGGGCGACCG GATGGCTATA GCTTGAGCAA	1080
TACGACCGCA TGACGAGCGG GACTCGGCG CCGCCCGTGC TCGCGTCCCG GCGCGCTCTG	1140
ACGGACCAAT CCGCTCTTTC TGTATTCACG CGACACGTGG ACCAAGATT CCGTACGGCC	1200
AGGTGGGACG TCGCGGCGCA TTCTCTGTCC TATACCAACA GTTCAGCGAG CAGATCTGGG	1260
CTCGCGCGCG CAACAGAAAG TCCTTGAAAA CGACCGCCAA GGTGGTGGCG GCGCGCTGT	1320
CGGAGCTACA TCGGATTCG GCGCTCTTC TGGTTTTTGT CGACCGAGCG ACTACAGTA	1380
AGGACAGCGC GATCGCTTGG ATCGCGCGCA GCGAGCTGAT GGTGACCTTA GCGAAGCTCG	1440
ACGGCAATG GCTGATACCG AAGTTACCG CCGTTAGGT TCGCGTAGCG GGTTCGCGAG	1500
TCTGACGGGG GCGCGGTGG CTCTCTGTCC GAGATACGG CCGTCTTCCG GACATCAAG	1560
GCGCGACTTC AAGAGATGT CCGCGCTGT GTAAATCGCC GGGTTATTTA AGATTAGTTC	1620
CGACTGTATT TACCTGATGT TCGATTTGTT CAGCTGGATT TACCTTGCGG GCGGAGCGGC	1680
TGGTGCACTT TGCATCTGGG GTTGAGACTA CTGAGAGAA TTTGACCTGT TCGGAGCTT	1740
GTTTCTCTGC CATCATGGGT GCTAGTTATG GCGGAGCGGA AGGATTATCG AATTCCTGGA	1800
CTTCGGGGCG TTACACCGCG AGATCAACTC CGCGAGATG TACCGCGGCC CGGATTCTGC	1860
CTCGCTGCTG GCGCGCGGGA AGATCTGGGA CAGGTGCGGG ATGAGCTGTG TTTGCGCGGC	1920
GTGCGGTTT CAGTGGTGG TCTCGGGTCT GACGACGGGA TCGTGGATAG GTTCGTGCGG	1980
GCGCTGATG GTGCGCGCG CCTGCGGTA TGTGGCTGGA ATGAGGCTCA CCGGAGGGGA	2040
GCGCGAGTGG AGGCGCGCG AGGTCCGGGT TCGTGGGGG GCTACGAGA CGGCGTATCG	2100
GTGACGCTG CCGCGCGCG TGATCGCGGA GAACCTGTCT GAATGATGA TTCTGATAG	2160
GACCGACCTC TTAGGCGAAA ACACCGCGCG GATCGCGCTC AACGAGCGCG ACTACGCGGA	2220
GTGTGGGCGC CAGGAGCGCG CCGGATGTT TCGCTACCGC GCGAGCGCG CGAGCGCGAC	2280
CGAGCGGCTG CTGCGCTTC AGGACCGCGC ACTGATACCG AACCGCGCG GGTCTCTTGA	2340
GCGCGCGCTC GCGTCHAGG AGGCGATCGA CACCGCGCGG GCGAACCACT TGATGACGAA	2400

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TGTGCTCCAA GCGGTGCAAC AACTGGGCTCA GCGCAGGAAA AGCATCTGGC CGTTCGACCA 2468
ACTGAGTGAA CTCTGGAAGG CCACTGCGCC GCATCTGTCS CCGGTCAGCA ACATGTTTC 2520
GATGCTCAAC AACCAAGGTG GATGACCAAA CTGGGGTGTG TCGATGGCCA GCACCTTGCA 2580
CTCAATGTTG AAGGGGTTG CTGGGGGCGG GGTTCAGAGG GTGGAAGCC GCGGCGAAAA 2640
CGGGGTCGAG GCGATGAGCT GCGTGGGCGG CAGCTGGGCT TCTGCGCTCG GTTCTTCGGG 2700
TCTGGGCGGT GGGGTGGGCG CCAACTTGGG TCGGGGCGCC TCGGTGTTT GGTTCGCTGT 2760
GGGCGAGGCG TGGGCGGCGG CCAAGCAGGC GGTCAAGCGG GGGGGGCGG GCGTGGGCT 2820
GACGAGCTG ACCAGGCGG CCAAGGCGG CCGCGGACAC ATGCTGGCG GGTTCAGGCT 2880
GGGGGAGCT ACCAATAGG GCGGCGGCTT CCGGGGCGTT AGCAATGCT TCGGATGCG 2940
GCGGGGCGG TACGATATG CCGGTGTGCG GCGGCGCGG TACGCGGAT CCGGACGCAA 3000
TGGGGGCGCT CTATCGGCGG AGCGATC 3060

```

(2) INFORMATION FOR SEQ ID NO:111:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: Linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1             5             10             15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20             25             30
Asp Ser Val Ala Ser Asp Leu Phe Ser His Ala Ser Ala Phe Gln Ser
35             40             45
Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
50             55             60
Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65             70             75             80
Ala Gly Gln Ala Glu Leu Thr Ala Ala Glu Val Arg Val Ala Ala
85             90             95
Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
100            105            110
Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
115            120            125
Glu Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met

```

136	137	140
Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala		
143	150	155
Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr		
	165	170
Asn Pro Gly Gly Leu Leu Glu Glu Ala Val Ala Val Glu Glu Ala Ile		
	180	185
Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu		
	195	200
Glu Gln Leu Ala Glu Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu		
	210	215
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn		
	225	230
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val		
	245	250
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala		
	260	265
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met		
	275	280
Ser Ser Leu Gly Ser Glu Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu		
	290	295
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser		
	305	310
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro		
	325	330
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr		
	340	345
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn		
	355	360
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro		
	370	375
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly		
	385	390

(2) INFORMATION FOR SEQ ID NO:112:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1616 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGAGGGG AGTGTATCCT ATGCTGTGGC AGCATATGCC ACCGAGTAA ATACGCCAGC	60
CTGTATGGGC GGGGGGGGTC CGGCTCAAT GCTTGGGGGG GCGCGGGAT GGCAGACGCT	120
TTGGGGGCT CTGGACGCTC AGGCCCTGCA GTTGACCGGT GCGCTGAAT CTCTGGGAGA	180
AGCTGGACT GGAGGTGGCA GCGACAGGGC GCTTGGGGCT GCACGCTCA TGGTGGCTG	240
GCACAAACG GCGTCAACAC AGGCAAGAC CCGTGGATG CAGGCGACGG CGCAAGCTGC	300
GGCATAACG CAGGCGATGG CCAGACGGCG GTCCGTGGCG GAGATGGCG CCACAGCAT	360
CACCGAGCC GTCCCTACGG CCACCAACTT GTTCGATC AACACGATC CGATCGGCTT	420
GACGAGATG GATTATTTCA TCCGATGTG GAACGAGGCA GCGCTGGCA TGGAGGTCTA	480
CCAGGCGGAG ACCGCGGTTA ACAGCGTTTT CGAGAAGCTC CAGCGGATGG GCTCGATGCT	540
TGATCGGCG GCGAGGCGCA GCGACGAGAA CCGATGCTT GGAATGCGCT CCGCTGGCAG	600
CTCAGACGG GTTGCGGCTT TGGGCGGGCG GGCTACCGAG ACCTCGGCG AACTGGGTGA	660
GATGACGGCG CCGATGCAAC AGCTGACCCA GCGGCTGGAG CAGGTGACCT GGTGTGCG	720
CCAGGTGGCG GGCACGGCG GCGGCAAGCG AGCGGAGGAG GAAGCGGCGC AGATGGGCTT	780
GCTGGGACG AGTGGGCTGT CGAAGCTATC GTGGCGTGGC GATGAGGCG CCAGCGGGCG	840
CGCGGGCGCT CTGGCGGGCG AGTGGCTACC TGGCGGAGT GGGTGGTGA CGCGGCGCG	900
GCTGATGCT CAGGTGATCG AAAGCGGGGT TGGCGGCTG GTGATGGCG GGGTGGCTG	960
CGATGCTGCG GCGAGGCTG GCGCGGCTG GGTGGGTCG GAGCGATGG GCGAGGCTG	1020
GCAATCGCG GCGTCAACCA GCGCGGCTGT GGTGGGTCG GCGCGGTCG GCGAGGCTG	1080
TGAGGAGAG GAGGAGGAGC AGTGGGAGCA AGAGGAGGAG TGGTGGCTC CCGATGATC	1140
AGCGGACTTC CGCGGACCG GCGCGGAGG ACTTGGGAG ATTTGGGCA GCGAGGTAAG	1200
GAGGAGAGGT ACTGAGGAT GCGAGAGATG AAGAGGAGT CCGGTACCT CCGGAGGAG	1260
CGAGGTAAT TGGAGCGGAT CTCGCGGAG CTGAAAGCC AGATGAGCA GGTGGAGTGG	1320
ACGGAGGTT CTTTGGAGG CGAGTGGCG GCGCGGCGG GAGCGGCGC CAGGCGCGCG	1380
GCGGTGGCT TCGAGAGAG AGCGATAGG CAGAGGAGG AACTGAGGA GATTCGAGG	1440
AATATGCTG AGCGCGGCT CCGATGCTG AGGCGGAGG AGGAGGAGCA GCGGCGGCTG	1500
TCTTGGCAA TGGCTTCTG ACCGCTAAT AGGAAAGAG AGGAGGCAA AACATGACG	1560
AGCAGAGTGG GATTTGCGG GGTATGAGG CCGCGGAGG CGCAATCGAG GGAAT	1616

## (2) INFORMATION FOR SEQ ID NO:113:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: Linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACATGGC CATTTCCTGC AGTCACACTG GCTTCCTGCT TCACATTTTG	40
GCACGCCGC GGAAACGAAG CACTGGGCTC GAGGACGGC TCGCTGACA TATGTCGGG	120
AGCTTCATA CTTTCCTGG GCGGAAGAG CTTCCTGTC TCGCGGCCA TGCACATTC	180
TGAGAGTGG CACAACTA TAAACACGAG AAGGCGGAG ACXAGCGAA GGTGGAATC	240
GCGGATCCC GTGTTGCT ATTCTAGCG AACTGGGCT TCCCTATGC GAACATCCA	300
CTGACGTTC GTTGGTCA AGCATTCGC TGAACGGCT CCGTATCGT CGGCGCGGG	360
TTCTGAGAG CGTTGTGAG CTCGTATGC GTGGCTGCC ATTTTCTG GACACCTGG	420
TACGCTCCG AA	432

(2) INFORMATION FOR SEQ ID NO:114:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Leu	Trp	Ser	Ala	Met	Pro	Pro	Glu	Asn	Thr	Ala	Arg	Leu	Met	1	5	10	15	
Ala	Gly	Ala	Gly	Pro	Ala	Pro	Met	Leu	Ala	Ala	Ala	Gly	Trp	Gln	20	25	30		
Thr	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu	Thr	Ala	Arg	35	40	45	
Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser	Asp	Lys	Ala	50	55	60	
Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr	Ala	Ser	Thr	65	70	75	80
Gln	Ala	Lys	Thr	Arg	Ala	Met	Glu	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	85	90	95	
Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Ala	Asn	100	105	110	
Ser	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe	Gly	Ile	Asn	115	120	125	

138

Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp  
 130 135 140  
 Asn Gln Ala Ala Leu Ala Met Gln Val Tyr Gln Ala Gln Thr Ala Val  
 145 150 155 160  
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro  
 165 170 175  
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro  
 180 185 190  
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr  
 195 200 205  
 Leu Gly Ala Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln  
 210 215 220  
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly  
 225 230 235 240  
 Gly Gly Asn Pro Ala Asp Gln Glu Ala Ala Gln Met Gly Leu Leu Gly  
 245 250 255  
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser  
 260 265 270  
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly  
 275 280  
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val  
 285 290 295 300  
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly  
 305 310 315 320  
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser  
 325 330 335  
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln  
 340 345 350  
 Glu Arg Glu Gln Asp Asp Gln Asp Asp Trp Asp Glu Glu Asp Asp Trp  
 355 360 365

## (2) INFORMATION FOR SEQ ID NO:115:

## (1) SEQUENCE CHARACTERISTICS:

- (a) LENGTH: 198 amino acids
- (b) TYPE: amino acid
- (c) STRADEDNESS:
- (d) TOPOLOGY: linear

## (2) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Gly Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly  
 1 5 10 15



```

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
    20                               25                               30
Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
    35                               40                               45
Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Gln Ala Ala Asn Lys
    50                               55                               60
Gln Lys Gln Glu Leu Asp Gln Ile Ser Thr Asn Ile Arg Gln Ala Gly
    65                               70                               75                               80
Val Gln Tyr Ser Arg Ala Asp Gln Gln Gln Gln Gln Ala Leu Ser Ser
    85                               90                               95
Gln Met Gly Phe
    100

```

## (2) INFORMATION FOR SEQ ID NO:116:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GATCTCGGAG GACCTGAGAA CCGAGATCGA CCGAGGTGAG TGGAGGCGAG GTTCGTTGCA      60
GGGCGCAGTGG CGCGCGGCGGG CCGCGACCGC CGGCCAGGCC GCGGTGGTGG GCTTCCGAGA      120
AGCAGCCAAAT AAGCAGAGGC AGGAAGTCCA CCGCATCTCG AGGAGTAATC CTCAGGCGCG      180
CGTCCAAATC TCGAGGAGCG AGGAGGAGCA GCGAGGCGCG CTGTCTCTCC AATGCGCTT      240
CTGACCGGCT AATAGAAAAA GAAACGGAGC AAAACATCGA CAGAGCGAGCA GTGGATTTTC      300
GCGGTAATCG AGGCGCGCGC AAGCGCAATC CAGCGAATGC TCAGTTCCTT TATTTCCTTC      360
CTTGAGGAGG GGAAGCAATC CCGACCAAG CTCGCA

```

## (2) INFORMATION FOR SEQ ID NO:117:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Phe Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala

```

140

1	5	10	15
Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala His Gln	20	25	30
Ala Ala Val Val Arg Phe Gln Gln Ala Ala Asn Lys Gln Lys Gln Gln	35	40	45
Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser	50	55	60
Arg Ala Asp Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe	65	70	75

## (3) INFORMATION FOR SEQ ID NO:118:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGATACCGG ATCCGCTGTT TGGCTATTCT AGCGAAGCTC GGGCTTGCCG TATGGAGACA	60
TGGAGTGTAC GTTGCATCTC GTGGAAGCCA TTGCTGACT GCTTGGGTG ATCGTCCGCG	120
CGAGTCTCTG CAGCGCTTTG TTGAGCTCGG TGGCGTGGC GTGCAATTT TCGTACACAC	180
CTGTGTACGC CTCGAGACCG CTACCGGCGC AGCGCGGTGC GAGCTTCTGC AGGCAATGCT	240
TGCGCTCTGC AAGGAGGAAA TGAATGAGC TGACATTTC CTGATATGCG GTTGGCGGCG	300
CTCGATACCG CGCGAATTC CAGTCTGCT CTGTGATGTT TTGCTCGCT TCTTTTCT	360
ATTAGAGGCT CAGAGGCCA TTTCGCA	387

## (2) INFORMATION FOR SEQ ID NO:119:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CAGCAGCAGG ATCTCGATTG GCCCAAGGCG GCTGGGAGAG GCTCCCTTCC GGGGGCAGG	60
TGGCGCGCGG ATGCTTCTCC TGCGCGCAGC CGCGCTCGCA TGGATGAGC AGTTGCTACG	120
TTGGGAGACT TTCTTTGGGT GTGTGTGCGA TAGCGGTGAC CCGGCGGCGC ACCCTCGAG	180

TGTTGAGGGG CAGGGGGGGT CGGTGGTTC GCGGGGAGC CAGACGGTCT GGACGGACG 249  
 GGGGGGGGT CCGCGATTGG CATGTTTGG CA 272

## (2) INFORMATION FOR SEQ ID NO:120:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val  
 1 5 10 15  
 Val Ala Ala Leu  
 20

## (2) INFORMATION FOR SEQ ID NO:121:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:122:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys  
 1 5 10 15  
 Glu Gly Arg

## (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Ile	Asp	Pro	Ala	Trp	Gly	Pro
1			5						10				15	

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Gly	Asp	Glu	Gln	Xaa	Ala	Val
1			5						10				

## (2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala	Gln	Glu	Ser	Ile	Ser	Tor	Xaa	Glu	Xaa	Ile	Val	Pro
1			5						10			

## (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro
1			3					10						15	
Ser															

(12) INFORMATION FOR SEQ ID NO:127:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala	Pro	Lys	Thr	Tyr	Asn	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1			5						10					15

(12) INFORMATION FOR SEQ ID NO:128:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1			5					10						15	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
		20						25					30		

(12) INFORMATION FOR SEQ ID NO:129:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp	Pro	Pro	Asp	Pro	Gln	Asn	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1			5					10						15